

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 04:30:38 ; Search time 6675 Seconds
(without alignments)
9871.076 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711.
Sequence: 1 AGCTTCATAGAACTCAA.....GATCTAGATTGTTCTGCGAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_ges_hum.*
18: em_ges_inv.*
19: em_ges_pin.*
20: em_ges_vrt.*
21: em_ges_fun.*
22: em_ges_mam.*
23: em_ges_mus.*
24: em_ges_pro.*
25: em_ges_rod.*
26: em_ges_pbg.*
27: em_ges_vrl.*
28: gb_ges1.*
29: gb_ges2.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.6	3.0	255	13	BQ280286
2	74.8	2.8	987	29	AL104456 Drosophill
3	69.6	2.6	1148	13	BX360752
4	66.2	2.4	1200	13	BX415878

5	66.2	2.4	1200	13	BX437758
6	65.4	2.4	488	13	BX424122
7	64.6	2.4	1124	13	BX436282
8	64.4	2.4	994	13	BX414650
9	61.8	2.3	1101	29	CNS0106X
10	61.4	2.3	1101	29	CNS00EVL
11	60.6	2.2	637	29	CNS036CC
12	60.6	2.2	928	29	CNS00DKY
13	60.4	2.2	1076	13	BX338020
14	60.2	2.2	1101	29	CNS0039G
15	59.4	2.2	1200	13	BX415878
16	59	2.2	994	13	BX414650
17	58.8	2.2	1201	9	AL536104
18	58.6	2.2	1201	13	BX461824
19	58.4	2.2	1059	13	BX442829
20	58.2	2.1	1201	13	BX335665
21	58	2.1	1165	13	BX338369
22	57.8	2.1	938	29	CNS006TJ
23	57.8	2.1	1027	29	CNS02T50
24	57.6	2.1	1201	13	BX458623
25	57	2.1	1201	13	BX421282
26	56.8	2.1	660	28	BH183498
27	56.8	2.1	660	29	CNS070XJ
28	56.8	2.1	1001	29	CNS01400
29	56.8	2.1	1101	29	CNS001FB
30	56.8	2.1	1225	29	CNS0161D
31	56.4	2.1	973	29	CNS0080F
32	56.2	2.1	1201	9	AL532464
33	56.2	2.1	1201	13	BX437779
34	56	2.1	427	13	BX403499
35	56	2.1	1101	29	CNS00ESI
36	56	2.1	1200	13	BX437739
37	56	2.1	1201	13	BX461310
38	55.8	2.1	1101	29	CNS0100X
39	55.6	2.1	1201	9	AL556024
40	55.4	2.0	1101	29	CNS00238
41	55.2	2.0	1101	29	CNS004ZW
42	55.2	2.0	1101	29	CNS016LI
43	55	2.0	1101	29	CNS003BD
44	55	2.0	1200	13	BX436510
45	55	2.0	1201	13	BX458623

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

BQ280286
PAC000000001474 Pioneer AF-1 array Zea mays CDNA, mRNA sequence.
BQ280286
BQ280286.1 GI:30270760
EST.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
Habben.J.
Analysis of gene expression in drought stressed maize
Unpublished
Contact: Habben J
Trait and Technology Development, Agronomic Traits
Pioneer Hi-Bred International, Inc.
7250 NW 62nd Ave., P.O. Box 552, Johnston, IA 50131-0552, USA
Tel: 515 270 4130
Fax: 515 334 4778
Email: jeffrey.habben@pioneer.com.
Location/Qualifiers
1..255
/organism="Zea mays"
/mol_type="mRNA"


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QY 99 GGCATATATGATATTTTATAAAATTTGTTACGTTTTCGTTATTTTTCATAGATGTGT 158
Db 954 ATDKKAKKATAAAWTKTKTAAAWMTTKTKATATTTTATTTATTTATTTATTTATTTATTT 895

QY 159 CATATGATTTAAATCGTGGTAAATGAAAGAACAGATATCAAACTATCAGAACTTTTGGTAGTTT 218
Db 894 ATTTTAAAKTATTTATAAABATTKGAAGABAAATTTAATATKATKAGATTTTTCATTK 835

QY 219 AATAAAAAACGGAGGTATTTTATGAGGAAATTAATCAAAATCAATGCATACCTTACAA 278
Db 834 KATAATKTKTKAWAAKDKTAAKTKKATAATTTTAAATKAACAADATDTATTK 775

QY 279 TTGTTTAACTTAACTCTGGAAGATCTTTTGGATGAGACGATATCAACTGGTATTA 338
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QY 339 CTCAATGATATTTCTGTCACCTGTTCTAGTTTCTGCTATCTAACTTTGTACACGGGG 398
Db 715 AAAAATTTTKTTTTTAAAAATTTATTTTATATATTTTAAATTAATATATKTTTWT 656

QY 399 AGGATTTTATGTTGGAATTAATAGATTTTGTATGCGGAATAGTTGGCCCTTCTCAATGGGA 458
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QY 459 TGCATTTCTAGTACAAATGAACAATTAATTAATGAAGATAGCTGAATTTCTAGGAA 518
Db 595 KTMGKTKTKMAATTKMAATTKMAAAGTTATKTKGGAATGAGAGATAAAATTTATMAMGG 536

QY 519 TGCTGCTATTTGCTAAATTTAGAGGATTTAGGAACAATTTCAATATATATGCGGAACATT 578
Db 535 MGGHAMMGMKMMATGTTGTTKMAATTAGTGGGAGGAATAKTTTAGATTAATTGAGGW 476

QY 579 TAAAGATGGAAGAGATCTCTAATAATCCAG 610
Db 475 TTATGATAGGGGATGATTTGGGATATGCG 444

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LOCUS
DEFINITION
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  5-PRIME, mRNA sequence.
ACCESSION
  BX415878
VERSION
  BX415878.1 GI:30765550
SOURCE
  Homo sapiens (human)
  EST.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1200)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 EVRY cedex - France
  Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID: CS0CAP008BE02QPI.
  Location/Qualifiers
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      /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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      the Not I and EcoRV sites of the pCMVSPORT 6 vector."

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      the Not I and EcoRV sites of the pCMVSPORT 6 vector."

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BASE COUNT      428 a      70 c      85 g      447 t      170 others
ORIGIN

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Best Local Similarity 35.7%; Pred. No. 0.078;
Matches 272; Conservative 101; Mismatches 379; Indels 9; Gaps 3;

QY 87 TTTTAAATATGGGGCATATATGATATTTTATAAAATTTTGTACGTTTTCGTTATTTT 146
Db 427 TTAAAAATTTTBBSSSTWATATTTTATTTTATATATTTTATTTWATTTTAAATTTT 486

QY 147 CATAGATGTCATATGATTTTAAATCGTGGTAAATGAAAGAACAGTATCAAACTATCAGAA 206
Db 487 AAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 546

QY 207 CTTTGTAGTTTAAATGAAAGAACGGAGGTATTTATGAGGAGGAAATTAATCAAAATCAATG 266
Db 547 TTTTATTTTAAATATTTTAAAGAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTT 606

QY 267 CATACCTTACAAATTTGTTTAAAGTAATCTCGAAGAGTACTTTTGGATGGAGACGGATATC 326
Db 607 TWTWTWTWTATTTTATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 666

QY 327 AACTGTAAATTAATCAATGATTTTCTCTGTCACCTGTTGTCAGTTTCTGGTATCTAATCT 386
Db 667 WTATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 726

QY 387 TGTACCAGGGGAGGAGTTTATGTTGATTAATAGATTTTGTATGGGATAGTTGGCC 446
Db 727 TTWAAAGAAATTAATTAATACATATATATATATATATATATATATATATATATATAT 786

QY 447 TTCTCAATCGGATGCAATTTCTAGTACAAATTCGAACAAATTAATTAATGAAAGATAGCTGA 506
Db 787 TATTTWAAATWACAAATWAAATWAAATWAAATWAAATWAAATWAAATWAAATWAAATW 840

QY 507 ATTGCTAGGAATGCTGCTATTTAGTAAATTTAGAGGATTTAGAAACAAATTTCAATATATA 566
Db 841 WAAATTTTAAAAAAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 900

QY 567 TCTGGAGAGCATTTA--AAGAATGGGAGAGAGATCTTAATATCCAGCACCAGCAGCA 624
Db 901 TTTTWTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 960

QY 625 GTAATTTGATCGCTTTCTGATATCTGATGGCTACTTTGAAAGGAGCAATCTCTCGTTT 684
Db 961 TTTTWWAAATWATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020

QY 685 ATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAGCGGCCAATCTGCATCTA 744
Db 1021 TWTWTAAAAAAATTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1079

QY 745 GCTATATTAAGAGATCTCTAATTTTGGAGAGAAAGATTTGGGATTTGCAACGATAATGTC 804
Db 1080 AWAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1139

QY 805 AATGAAATCTAATAAGACTAATTTAGGCAATTTTATGATGAATA 845
Db 1140 AATTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1180

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RESULT 5
BX437758
LOCUS
DEFINITION
  BX437758 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YB01
  5-PRIME, mRNA sequence.
ACCESSION
  BX437758
VERSION
  BX437758.1 GI:30773605
KEYWORDS
  EST.
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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5-PRIME, mRNA sequence.
BX424122
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 488)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0CAP008CA010P1.
Contact: Genoscope
Location/Qualifiers
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6569.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE002F08QPI&cluster=6569.f. Contact :
Feng Liang Email : fliang@lifetech.com URL : Corporation 1600
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DE002F08QPI.
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
Library 2 c 39 g 161 t 84 others
BASE COUNT 202 a 2 c 39 g 161 t 84 others
ORIGIN -
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Best Local Similarity 41.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 171; Conservative 35; Mismatches 211;
QY 85 AATTTTAAATATGGGCGCATATATGATATTTTATATAATTTTGTACGTTTGTGTTT 144
DB 30 AATTTTATATTTTATATATTTTATATTTTATTTTATTTTATTTTATTTTATTTT 89
QY 145 TTCAATACATGCTCATATGATTAATCGTGAATGAAACAGATATCAAACTATCAG 204
DB 90 TATTTTAAATTTATATATATATATTTTATATAAATTAATAAATAATAATTAATAAT 149
QY 205 AACTTTGGTATTTTATATAAAGCGGATTTTATGAGGAAATATCAAAATCAA 264
DB 150 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 209
QY 265 TCATPACCTTACATTTTAAATGATATCTCTGAAGAAGTACTTTTGGATGAGAACGATA 324
DB 210 AAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 269
QY 325 TCAACTGGTATTAATCAATGATATTTCTCTGCTCAGTTTCTGTTTCTGTTTCTGTT 384
DB 270 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 329
QY 385 TTTGTACACAGGGGAGGATTTTATGTTGATTAATAGATTTTGTATGGGGAATGTGGC 444
DB 330 TTTGTGCTGG 389
QY 445 CTTTCTCAATGGGATGATTTCTAGTACAAATTTGAACAAATTAATTAATGAAGAATA 501
DB 390 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 446

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0CAP008CA010P1.
Contact: Genoscope
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/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."
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BASE COUNT 515 a 30 c 71 g 310 t *274 others
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Query Match 2.4%; Score 66.2; DB 13; Length 1200;
Best Local Similarity 28.5%; Pred. No. 0.078;
Matches 143; Conservative 130; Mismatches 225; Indels 3; Gaps 1;
QY 72 AACATAATCGGTCAATTTAAATATGGGCGATATATGATATTTTATAAATTTGTTACG 131
DB 278 AWWAAATTTTAAATATWDGATKADATTGGGGGDMTTTWWTTTAAARRDKTTTTT 337
QY 132 TTTTGTATTTTTCATAGATGTGCATATGATTAATCGTGAATGAAACAGT 191
DB 338 TTTTAAATATATKGGGGGADATATTTTATTTTATTTTATTTTATTTTATTTTATTT 397
QY 192 ATCAAACTATCAGAACTTTGGTAGTTTAAATAAAGGAGGATTTTATGAGGAAAA 251
DB 398 TTTTWWAGGARKDGTDTTAAADWWTTTAAAWWWNDKRTTTTTTTTTTGGRAAAAT 457
QY 252 TAATCAAAATCAATGCATACCTTACAAATTTTAAAGTAACTCTGAAGAAGTACTTTGGA 311
DB 458 TTTTTTTTTTTAAKAAAAAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 517
QY 312 TGGAGACGGATATCACTGTAATTTCTCAATGATTTTCTGTCATTTGTCAGTT 371
DB 518 TTAATWWGGAGRTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 577
QY 372 TCTGTATCTAATCTTCTACAGGGGAGGATTTTATGTTGATTAATAGATTTTGTATG 431
DB 578 AAGAGAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 637
QY 432 GGGAAATGTTGCCCTTCTCAATGGATGCTATTTCTAGTACAAATTTGAACAAATTAATA 491
DB 638 TTTTTTTTTTTGTCTTTTAAAGGATTTTATTTTATTTTATTTTATTTTATTTTATTT 697
QY 492 TGAAGAATAGCTGAATTTGCTAGGATCTGCTATT---GCTAATTTAGAGGATTAGS 548
DB 698 WTAAAWAAWAAAGAAAGAAAGAAATTTTATKAGARRGATTTTAAATTTTAAATTTT 757
QY 549 AAACAATTTCAATATATATGT 569
DB 758 ARGADTTTTTATATTTTATTT 778

RESULT 6
BX424122
LOCUS
DEFINITION
BX424122 Homo sapiens PLACENTA cDNA clone CS0DE007YB10
linear EST 13-MAY-2003


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RESULT 7
BX436282      1124 bp mRNA linear EST 15-MAY-2003
LOCUS        BX436282 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001Y01
DEFINITION   5-PRIME, mRNA sequence.
ACCESSION    BX436282
VERSION      BX436282.1 GI:30787521
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 1124)
JOURNAL      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT      Full-length cDNA libraries and normalization
              Unpublished
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Paraday Avenue Genoscope sequence ID : CS0CAP001AB01QPI.
              Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="CS0CAP001Y01"
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                /clone_lib="Homo sapiens THYMUS"
                /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
                with a NotI-oligo(dT) primer. Five prime end enriched,
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                the NotI and EcoRV sites of the pCMVSPORT 6 vector.
                Library was not normalized."
BASE COUNT   129 a 29 c 109 g 435 t 422 others
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Query Match      2.4%; Score 64.6; DB 13; Length 1124;
Best Local Similarity 23.3%; Pred. No. 0.15;
Matches 115; Conservative 160; Mismatches 218; Indels 0; Gaps 0;
QY 87 TTTTAAATATGGGCATATATGATATTTTATAAAATTTGTTACGTTTTTGTATTTTTT 146
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QY 147 CATAAGATGTCATATGATTAATAATCGTGGTAAATGAAACAGTATCAAACTATCAGAA 206
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QY 207 CTTTGTAGTTTATAAAAAACGGAGGTATTTTATGGAGGAAAAATATCAAAATCAATG 266
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QY 327 AACTGGTAATCTCAATGATATTTCTCTGTCACCTGTGTCAGTTTCTGGTATCTAATCT 386
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QY 387 TGTACACGGGGAGGATTTTGTAGTGAATATAGATTTTGTATGGGATAGTTCGCC 446
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QY 447 TTCTCAATGGATGTCATTTCTAGTACAAATTAATTAATTAATTAATTAATTAATTA 506
Db 824 TTTTTRRRRRRRRTTTTTTTTTTTTTTTTTTTTTTTTTTTTDDRRRRRTTTTTTDD 883
QY 507 ATTTGCTAGGAATGCTGCTATTGCTAATTTAGAAGGATTAGGAAACAAATTTCAATATA 566

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Db 884 RRDDTTTTTTTDTTDTTDTTDTTDTTDTTDDDDDTTDTTDRRRRTTTRRRRRRRRRRRRRRTT 943
QY 567 TGTGGAAGCATTT 579
Db 944 TDRRRRRRTTTT 956

RESULT 8
BX414650/c
LOCUS        BX414650 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YN02
DEFINITION   3-PRIME, mRNA sequence.
ACCESSION    BX414650
VERSION      BX414650.1 GI:30763455
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 994)
JOURNAL      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT      Full-length cDNA libraries and normalization
              Unpublished
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 6015.f
              Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0CAP001DG01NP1.
              Location/Qualifiers
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                /organism="Homo sapiens"
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                /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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                the NotI and EcoRV sites of the pCMVSPORT 6 vector.
                Library was not normalized."
BASE COUNT   185 a 121 c 25 g 324 t 339 others
ORIGIN
Query Match      2.4%; Score 64.4; DB 13; Length 994;
Best Local Similarity 22.4%; Pred. No. 0.17;
Matches 120; Conservative 184; Mismatches 227; Indels 4; Gaps 1;
QY 71 GAACATAATCGTGCAATTTTAAATATGGGCATATATGATGATATTTTATAAAATTTGTTAC 130
Db 906 GDDWDWDTATWWAADDWAAARWAAATWTTDWTATWTRKDKATWKADDDDDAKTKTT 847
QY 131 GTTTTGTGTTATTTTTCATAGATGTCATATGATGATTAATAATCGTGGTATGAAACAG 190
Db 846 TTTTWTWKAATWDAGTAKWADATWADAADAWAARAWAAARAWAAARAWAAADADWW 787
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Db 666 RKDDARDDDWAAWTTTTTTTTTTTAAWAADKAWKKWKTATTTTTTTTTTTTTTTT 607

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The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila* Aaron Mammoser BAC library was prepared by Kazutoyo Oseogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila/bac.htm>.

FEATURES

[illegible]

Db
437 WTWTWAAATTAATTTTWTAAAAAAWWTWTATA 397

RESULT 15
BX415878/c

LOCUS	EX415878	1200 bp	linear	EST 15-MAY-2003
DEFINITION	EX415878 Homo sapiens THYMUS cDNA clone CS0CAP008Y104			
DESCRIPTION	5'-PRIME, mRNA sequence.			
ACCESSION	EX415878			
VERSION	EX415878.1	GI:30765550		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			

SOURCE
ORGANISM

Chordata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa;
Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 1200)
AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
COMMENT
Contact: Genoscope

CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifestech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOCAP008BE02QPI.

FEATURES

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/note="Vector: pCMVSPORT 6; 1st strand cDNA with a NotI-oligo(dT) primer. Five prime double-strand cDNA was digested with NotI. The Not I and EcoRV sites of the pCMVSPORT Library was not normalized."
428 a 70 c 85 g 447 t 170 others
BASE COUNT
ORIGIN

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Query Match	2.2%	Score 59.4	DB 13	Length 1200
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Db	839	TTTTTAAATTTAAWAAWTTTTTA--AAWTTTTTTTAAWTTTGTWATTTWAAATATTTAAW	782	
QY	325	TCAACTGGTAAATTAATCAATTCGATATTTCTCTGTCACCTTTGTCAGTTTCTGGTATCTAAC	384	
Db	781	TAAWATWATATTTATGHWTTATATATATATNTATGTAATTAATWTTTCTTTTAAWAAAAWT	722	
QY	385	TTTGTACCAAGGGGGGATTTTTAGTTGGATTAATAGATTTTTTGTATGGGGAATAGTTGGC	444	
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us-09-918-485-1.rst

Wed Oct 15 11:56:16 2003

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Search completed: October 13, 2003, 10:12:43
Job time : 6683 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 08:21:18 ; Search time 2257 Seconds
(without alignments)
3116.763 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711
Sequence: 1 AGCTTCATAGATCTCAA.....GATCTAGATTGTTCTGCGAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PTC_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2427.8	89.6	3567	11	US-09-972-175-9
7	2426.2	89.5	3567	11	US-09-972-175-7
8	2419.8	89.3	3567	11	US-09-972-175-58
9	2418.2	89.2	3567	11	US-09-972-175-60
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11	1498.2	55.3	3579	9	US-09-873-873-29
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ALIGNMENTS

RESULT 1

US-09-918-485-1
; Sequence 1, Application US/09918485
; Publication No. US20030115628A1
; GENERAL INFORMATION:

APPLICANT: SANCHIS, Vincent
LERECLUS, Didier
MENOU, Ghislaine
LECADET, Marguerite-Marie
MARTOURET, Daniel
DEDONDER, Raymond

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
LEPIDOPTERA

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,485
FILING DATE: 25-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: EP 88 401 121.4

FILING DATE: 06-MAY-1988		721		GCTCAAGCGGCAATCTGCACTAGCTATATAAGAGATCTGTAAATTTTGGGAAGA		780
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TELEPHONE: (703) 836-6620		Db		ACGTATCAAGATTTGGATAACATATAATCGAATTCAGGAGAGACTTAACATTTGCTGTATTA		960
TELEFAX: (703) 836-2021		Qy		GNTATCGCGCTTTCTTTCCAAATCTATGACATAGAGATATCAATTCAGCCAGTTCGT		1020
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Qy 2461 TATTTATATCAGAAATAGATGAGTGAATTTAAAGCTTTATACCGTTATGAATTAAGA 2520
Db 2461 TATTTATATCAGAAATAGATGAGTGAATTTAAAGCTTTATACCGTTATGAATTAAGA 2520
Qy 2521 GGTATATCGAATAGTCAAGACTTAGAAATCTATTGATCGCGTACAGTGCAGAACAC 2580
Db 2521 GGTATATCGAATAGTCAAGACTTAGAAATCTATTGATCGCGTACAGTGCAGAACAC 2580
Qy 2581 GAAATAGTAATGTGCGAGGACCGGTTCTTTATGCGCGCTTTTCAGCCCAAAAGTCCAAATC 2640
Db 2581 GAAATAGTAATGTGCGAGGACCGGTTCTTTATGCGCGCTTTTCAGCCCAAAAGTCCAAATC 2640
Qy 2641 GGAAGTGTGAGAACCGAATGATGCGGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
Db 2641 GGAAGTGTGAGAACCGAATGATGCGGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
Qy 2701 TGTTCTGCGAG 2711
Db 2701 TGTTCTGCGAG 2711

RESULT 2

US-09-972-175-1

; Sequence 1, Application US/09972175

; Publication No. US20030101482A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; Gilmier, Amy Jelen

; Mettus, Anne-Marie Light

; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING

; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-972-175-1

Query Match 89.6%; Score 2429.4; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0; Mismatches 26; Indels 0; Gaps 0;
Matches 2445; Conservative 0;

Qy 241 ATGGAGGAAAAATAACAAATCAATGCATACCTTAACTTTTAAAGTAATCCTGAAGAA 300
Db 1 ATGGAGGAAAAATAACAAATCAATGCATACCTTAACTTTTAAAGTAATCCTGAAGAA 60
Qy 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTTGATATTTCTGTCA 360
Db 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATTAATCAATTTGATATTTCTGTCA 120
Qy 361 CTGTGTTTCAAGTTTCTGATATCTAACTTTTGTACCAGGGGGAGGATTTTGTAGTGGATTAATA 420
Db 121 CTGTGTTTCAAGTTTCTGATATCTAACTTTTGTACCAGGGGGAGGATTTTGTAGTGGATTAATA 180
Qy 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 480
Db 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 240
Qy 481 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 540
Db 241 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 300
Qy 541 GGATTAGGAACAATTTCAATATATATGTTGGAAGCATTTAAAGATGGGAAGAATCCT 600
Db 301 GGATTAGGAACAATTTCAATATATATGTTGGAAGCATTTAAAGATGGGAAGAATCCT 360
Qy 601 AATATCCAGCAACCCAGGACAGAGTAATTTGATCGCTTTTGTATATCTTGTAGTGGCTACTT 660
Db 361 AATATCCAGCAACCCAGGACAGAGTAATTTGATCGCTTTTGTATATCTTGTAGTGGCTACTT 420
Qy 661 GAAAGGACATTTCTTCTGTTTTCGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 720

Db	421	GAAGGAGACATTCCTTCGTTGGCAATTTCTGGATTTGAGTACCCCTTTTATCGTTTAT	480	Qy	1801	TTAAGANTTCGTTACGCTTCCAGTAGGAGTCAGCAGTATTATAGTATTAAACAGAGCGGCA	1860
Qy	721	GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGATTCGTATTTTTCGAGGAAGA	780	Db	1561	TTAAGANTTCGTTACGCTTCCAGTAGGAGTCAGCAGTATTATAGTATTAAACAGAGCGGCA	1620
Db	481	GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGATTCGTATTTTTCGAGGAAGA	540	Qy	1861	TCACAGAGTGGGAGGCCCAAGTATTAGTATAGATATCCCTCTTCAGAAAACTATGGAAATA	1920
Qy	781	TTGGGATTGACAAAGATAAATGTCATGAAATCTAATATAGACTAATTAGGCATATTGAT	840	Db	1621	TCACAGAGTGGGAGGCCCAAGTATTAGTATAGATATCCCTCTTCAGAAAACTATGGAAATA	1680
Db	541	TGGGGATTGACAAAGATAAATGTCATGAAATCTAATATAGACTAATTAGGCATATTGAT	600	Qy	1921	GGGGAGAACTTTAATCATCTAGAACATTTAGATATATACCGAATTTTAGTAATCTCTTTTCAAT	1980
Qy	841	GAATATGCTGATCACTGTGCAAAATACGTATATCGGGGATTAATAATTTACCGAAATCT	900	Db	1681	GGGGAGAACTTTAATCATCTAGAACATTTAGATATATACCGAATTTTAGTAATCTCTTTTCAAT	1740
Db	601	GAATATGCTGATCACTGTGCAAAATACGTATATCGGGGATTAATAATTTACCGAAATCT	660	Qy	1981	AGAGCTAATCCAGATATATTTGGGATAAGTCAACCACTCTATTTGGTGACAGTTCAT	2040
Qy	901	ACGTATCAAGATTGGATAACAATATATCGATTACGGAGACTTAACATTTGACTGTATTA	960	Db	1741	AGAGCTAATCCAGATATATTTGGGATAAGTCAACCACTCTATTTGGTGACAGTTCAT	1800
Db	661	ACGTATCAAGATTGGATAACAATATATCGATTACGGAGACTTAACATTTGACTGTATTA	720	Qy	2041	AGTACGGTGAATCTTATATAGATAAATTCGAATTTATCTAGCAGATGCAACATTTGAA	2100
Qy	961	GATATCGCGCTTCTTTCCAAATGATGACAAATAGAGATATCAATTCAGCCAGTTGGT	1020	Db	1801	AGTACGGTGAATCTTATATAGATAAATTCGAATTTATCTAGCAGATGCAACATTTGAA	1860
Db	721	GATATCGCGCTTCTTTCCAAATGATGACAAATAGAGATATCAATTCAGCCAGTTGGT	780	Qy	2101	GCAGAACTCGATTAGAAAGACCAAAAGCGGCTGAATGCCCTTTACTTTCTTCCAAT	2160
Qy	1021	CAACTAACAGGAGGATTTATAGGACCCATTAATTAATTTAATCCAGTTACAGTCT	1080	Db	1861	GCAGAACTCGATTAGAAAGACCAAAAGCGGCTGAATGCCCTTTACTTTCTTCCAAT	1920
Db	781	CAACTAACAGGAGGATTTATAGGACCCATTAATTAATTTAATCCAGTTACAGTCT	840	Qy	2161	CAAACTCGGTTAAAAACCGATGTGACGGATTATCATATTGATCCAAATTTAGTG	2220
Qy	1081	GTAGCTCAATACCTACTTTTAACTGTTAGGAGACGCGCAATTAAGAATCCTCATTTA	1140	Db	1921	CAAACTCGGTTAAAAACCGATGTGACGGATTATCATATTGATCCAAATTTAGTG	1980
Db	841	GTAGCTCAATACCTACTTTTAACTGTTAGGAGACGCGCAATTAAGAATCCTCATTTA	900	Qy	2221	GATTGTTATCAGATGAATTTTCTGTGGATGAAAGCGAGANTTGTCCGAGAAAGTCAAA	2280
Qy	1141	TTTGATATATGATTAATCTTAACATCTTACGATTTAGGATTTAGTGTGAGCGCAATTT	1200	Db	1981	GATTGTTATCAGATGAATTTTCTGTGGATGAAAGCGAGANTTGTCCGAGAAAGTCAAA	2040
Db	901	TTTGATATATGATTAATCTTAACATCTTACGATTTAGGATTTAGTGTGAGCGCAATTT	960	Qy	2281	CATCGCAACCGACTCAGTGATGAGCGGAAATTTACTTCAAGATCCAACTTCAGAGGATC	2340
Qy	1201	TATTGGGAGGACATCGAGTAAATCTAGCTTTATAGAGTGTGATACATATCTCT	1260	Db	2041	CATCGCAACCGACTCAGTGATGAGCGGAAATTTACTTCAAGATCCAACTTCAGAGGATC	2100
Db	961	TATTGGGAGGACATCGAGTAAATCTAGCTTTATAGAGTGTGATACATATCTCT	1020	Qy	2341	AAATAGCAACACAGACCGTGGCTGGAGAGGAGTACAGATATTACCATCCAGAGGAGAT	2400
Qy	1261	ATATATGGAAGAGAGCGGCAACGAGGAGCTTCAAGATCTTTTATGAGCGGTA	1320	Db	2101	AAATAGCAACACAGACCGTGGCTGGAGAGGAGTACAGATATTACCATCCAGAGGAGAT	2160
Db	1021	ATATATGGAAGAGAGCGGCAACGAGGAGCTTCAAGATCTTTTATGAGCGGTA	1080	Qy	2401	GACGTATTCAAAGAGAAATTTAGTCACTACCGGTACCGTTGATGAGTGTCTATCCAAAG	2460
Qy	1321	TTTAGGACTTTATCAATCTCTACTTTAGATTTATACAGCAACCTTCCAGCGCCACAT	1380	Db	2161	GACGTATTCAAAGAGAAATTTAGTCACTACCGGTACCGTTGATGAGTGTCTATCCAAAG	2220
Db	1081	TTTAGGACTTTATCAATCTCTACTTTAGATTTATACAGCAACCTTCCAGCGCCACAT	1140	Qy	2461	TATTTATATCAGAAAAATAGATGAGTCCGAAATTTAAAGCTTATACCCGTTATGAATTAAGA	2520
Qy	1381	TTTAAATTTAGCTGGTGAAGGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT	1440	Db	2221	TATTTATATCAGAAAAATAGATGAGTCCGAAATTTAAAGCTTATACCCGTTATGAATTAAGA	2280
Db	1141	TTTAAATTTAGCTGGTGAAGGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT	1200	Qy	2521	GGGTATATCGAAGATAGTCAAGACTTAGAAATCTTATTTGATCGGTACAAATGCAAAACAC	2580
Qy	1441	GCAGGAAGAGTACGGTTGATTTCTTAACTGAATTTACCGCTGAGGATATAGTGTGCA	1500	Db	2281	GGGTATATCGAAGATAGTCAAGACTTAGAAATCTTATTTGATCGGTACAAATGCAAAACAC	2340
Db	1201	CGAGGAAGAGTACGGTTGATTTCTTAACTGAATTTACCGCTGAGGATATAGTGTGCA	1260	Qy	2581	GAATATGATTCGCGAGGACCGGTTCTTATGCGGCTTTCAGCCCAAAAGTCCAAATC	2640
Qy	1501	CCTCGGAAGATATAGTATCATCGTTTATGTCAGCAACTTTTGTTCAGAGATCTGGAACA	1560	Db	2341	GAATATGATTCGCGAGGACCGGTTCTTATGCGGCTTTCAGCCCAAAAGTCCAAATC	2400
Db	1261	CCTCGGAAGATATAGTATCATCGTTTATGTCAGCAACTTTTGTTCAGAGATCTGGAACA	1320	Qy	2641	GAATATGATTCGCGAGGACCGGTTCTTATGCGGCTTTCAGCCCAAAAGTCCAAATC	2700
Qy	1561	CCTTTTAACTGCTGTAGTATTTCTTGGACGATCTGATGCAACTCTTTCATCAAT	1620	Db	2401	GAATATGATTCGCGAGGACCGGTTCTTATGCGGCTTTCAGCCCAAAAGTCCAAATC	2460
Db	1321	CCTTTTAACTGCTGTAGTATTTCTTGGACGATCTGATGCAACTCTTTCATCAAT	1380	Qy	2701	TGTTTCTGCGAG	2711
Qy	1621	ACATTTGATTCAGAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGAGTTTGGGG	1680	Db	2461	TGTTTCTGCGAG	2471
Db	1381	ACATTTGATTCAGAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGAGTTTGGGG	1440				
Qy	1681	GGCACCCTCTGATTCAGAGAGGAGATTTACAGGGGATATCTTTCGAAGAAATACC	1740				
Db	1441	GGCACCCTCTGATTCAGAGAGGAGATTTACAGGGGATATCTTTCGAAGAAATACC	1500				
Qy	1741	TTTGGGATTTTGTATCTCTACAGTCAATTAATTCACCAATACCAAGATACCT	1800				
Db	1501	TTTGGGATTTTGTATCTCTACAGTCAATTAATTCACCAATACCAAGATACCT	1560				

RESULT 3
US-09-972-175-11
; Sequence 11, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen

601 AATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTCGTATACCTTGATGGGTACTTT 660
Db AATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTCGTATACCTTGATGGGTACTTT 420
661 GAAAGGACATCTCTTTCGTTTCGAAATTCCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 720
Db GAAAGGACATCTCTTTCGTTTCGAAATTCCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 480
721 GCTCAAGCGCCCAATCTGCATCTAGCTATATTAAGAGATTCGTGTAATTTTGGAGAAAGA 780
Db GCTCAAGCGCCCAATCTGCATCTAGCTATATTAAGAGATTCGTGTAATTTTGGAGAAAGA 540
781 TTGGGATTCACACGATTAATGTCAATGAATACTAATAGACTAATTAAGGCATATTGAT 840
Db TTGGGATTCACACGATTAATGTCAATGAATACTAATAGACTAATTAAGGCATATTGAT 600
841 GAATATGCTGATCACTGTGCAATACGTATAATTCGGGGATTAATAATTTTACCGAATCT 900
Db GAATATGCTGATCACTGTGCAATACGTATAATTCGGGGATTAATAATTTTACCGAATCT 660
901 ACGTATCAAGATTTGGATTAACATATAATCGATTACGGAGAGACTTAACATTTGACTGTATTA 960
Db ACGTATCAAGATTTGGATTAACATATAATCGATTACGGAGAGACTTAACATTTGACTGTATTA 720
961 GATATCGCGCTTCTTTCCAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGT 1020
Db GATATCGCGCTTCTTTCCAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGT 780
1021 CAACTAAAGGAGAGTTTATACGGACCAATTAATTTTAAATCCACAGTTTACAGTCT 1080
Db CAACTAAAGGAGAGTTTATACGGACCAATTAATTTTAAATCCACAGTTTACAGTCT 840
1081 GTAGTCAATTTACTTCTTAACTGATGAGAGAGCGCAATAGAAATCTCATTTA 1140
Db GTAGTCAATTTACTTCTTAACTGATGAGAGAGCGCAATAGAAATCTCATTTA 900
1141 TTTGATATTAATTAATCTTACAACTTTTACGATTTGTTAGTTGGAGCGCAATTTT 1200
Db TTTGATATTAATTAATCTTACAACTTTTACGATTTGTTAGTTGGAGCGCAATTTT 960
1201 TATTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGGTAACATACTCTCT 1260
Db TATTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGGTAACATACTCTCT 1020
1261 ATATATGGAAGAGAGCGCAACAGGAGCCTCCAAGATCTTTTAACTGGACCGGTA 1320
Db ATATATGGAAGAGAGCGCAACAGGAGCCTCCAAGATCTTTTAACTGGACCGGTA 1080
1321 TTTAGACTTTTATCAATTCCTTCTTAACTGATTAACAGCAACCTTGCAGCGCCACCAT 1380
Db TTTAGACTTTTATCAATTCCTTCTTAACTGATTAACAGCAACCTTGCAGCGCCACCAT 1140
1381 TTTAATTTACGTTGGTCAAGGAGTATGATTTTCTTACACCTTACAAATAGCTTTACGTAT 1440
Db TTTAATTTACGTTGGTCAAGGAGTATGATTTTCTTACACCTTACAAATAGCTTTACGTAT 1200
1441 GCAGGAAGAGGTACGGTTGATTTCTTAACTGAATTAACCGCTTACAGGATTAATAGTTGCCA 1500
Db GCAGGAAGAGGTACGGTTGATTTCTTAACTGAATTAACCGCTTACAGGATTAATAGTTGCCA 1260
1501 CCTCGGAAGGATATAGTCAATCGTTTATGTCATGCAATTTTGTTCGAAAGATCTGGAACA 1560
Db CCTCGGAAGGATATAGTCAATCGTTTATGTCATGCAATTTTGTTCGAAAGATCTGGAACA 1320
1561 CCTTTTAACTGGTGTAGTATTTCTTGGAGCATCTGAGTGCACCTCTTCAAT 1620
Db CCTTTTAACTGGTGTAGTATTTCTTGGAGCATCTGAGTGCACCTCTTCAAT 1380
1621 ACAATTTGATCCAGAGAGATTAATCAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG 1680
Db ACAATTTGATCCAGAGAGATTAATCAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG 1440
1681 GGCACCTCTGTCTATTACAGGACAGAGTTTACAGGAGGGGATATCTTTCGAAAGAAATACC 1740

RESULT 5

Wed Oct 15 11:56:12 2003

US-09-972-175-5
; Sequence 5, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-972-175-5
Query Match 89.6%; Score 2427.8; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2444; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 241 ATGGAGGAATATCAAAATCAATGCATACCTTACAAATTTGTTTAAAGTAATCTCTGAAGAA 300
DB 1 ATGGAGGAATATCAAAATCAATGCATACCTTACAAATTTGTTTAAAGTAATCTCTGAAGAA 60
QY 301 GTACTTTTGGATCGAGACGGATATCAATCTGTAATTTACTCAATTTGATATTTCTCTGTCA 360
DB 61 GTACTTTTGGATCGAGACGGATATCAATCTGTAATTTACTCAATTTGATATTTCTCTGTCA 120
QY 361 CTGTGTCAGTTTCGGTATCTAATCTTGTACCGGGGAGGATTTTAAAGTGGATTAATA 420
DB 121 CTGTGTCAGTTTCGGTATCTAATCTTGTACCGGGGAGGATTTTAAAGTGGATTAATA 180
QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATCTTCTAGTACAAATTTGAA 480
DB 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATCTTCTAGTACAAATTTGAA 240
QY 481 CAATTAATTAATGAAGAATAGTCTGAATTTGCTAGGATCTCTGCTAATTTAGAA 540
DB 241 CAATTAATTAATGAAGAATAGTCTGAATTTGCTAGGATCTCTGCTAATTTAGAA 300
QY 541 GGATTAGGAACAATTTCAATATATATATGTGGAGCAATTTAAAGATGGGAAGATCTCT 600

301 GGATTAGGAACAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAAGATCTCT 360
QY 601 AATAATCCAGCAACACAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGCTACTT 660
DB 361 AATAATCCAGCAACACAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGCTACTT 420
QY 661 GAAAGGGACATTTCTTTCGTTTCGAAATTTCTGGATTTTGAAGTACCCCTTTATCCGTTTAT 720
DB 421 GAAAGGGACATTTCTTTCGTTTCGAAATTTCTGGATTTTGAAGTACCCCTTTATCCGTTTAT 480
QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTGGGATTTGACAAGCAATTAATGTCAATCAAAATCTATAATAGACTAATTAGGCATATTGAT 840
DB 541 TTGGGATTTGACAAGCAATTAATGTCAATCAAAATCTATAATAGACTAATTAGGCATATTGAT 600
QY 841 GAATATGCTGATCACTGTCGCAATAGCTATATTCGGGGATTTAAATAATTTTACCGAAATCT 900
DB 601 GAATATGCTGATCACTGTCGCAATAGCTATATTCGGGGATTTAAATAATTTTACCGAAATCT 660
QY 901 ACCTATCAAGATTTGGATAACAATTAATCGATTCGAGAGACTTAACATTTGACTGTATTA 960
DB 661 ACCTATCAAGATTTGGATAACAATTAATCGATTCGAGAGACTTAACATTTGACTGTATTA 720
QY 961 GATATCGCGCTTTCTTCCAAATAGCAATAGAGATATCCAAATTCAGCCAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTCCAAATAGCAATAGAGATATCCAAATTCAGCCAGTTGGT 780
QY 1021 CAATCAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCAGCTACAGTCT 1080
DB 781 CAATCAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCAGCTACAGTCT 840
QY 1081 GTAGCTCAATTTACCTACTTTTAAAGCTTTTACGGATTTGTTTGTGGAGCGCAATTTT 1140
DB 841 GTAGCTCAATTTACCTACTTTTAAAGCTTTTACGGATTTGTTTGTGGAGCGCAATTTT 900
QY 1141 TTGATATATTTGAATAATCTTTACAACTTTTACGGATTTGTTTGTGGAGCGCAATTTT 1200
DB 901 TTGATATATTTGAATAATCTTTACAACTTTTACGGATTTGTTTGTGGAGCGCAATTTT 960
QY 1201 TATTGGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGTGGTAAACATAATCTCT 1260
DB 961 TATTGGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGTGGTAAACATAATCTCTCT 1020
QY 1261 ATATATGGAAGAGGCGAACCAGGAGCCTCCAAAGATCTTTTACTTTTAAATGGACCGGTA 1320
DB 1021 ATATATGGAAGAGGCGAACCAGGAGCCTCCAAAGATCTTTTACTTTTAAATGGACCGGTA 1080
QY 1321 TTTAGGACTTTTATCAATTTCTTACTTTTACGATTTATACAGCAACCTTCCAGCGCCACCAT 1380
DB 1081 TTTAGGACTTTTATCAATTTCTTACTTTTACGATTTATACAGCAACCTTCCAGCGCCACCAT 1140
QY 1381 TTTTAAATTTAGCTGGTGAAGGATAGTAATTTTCTACACCTTACAAATAGCTTTTAGTAT 1440
DB 1141 TTTTAAATTTAGCTGGTGAAGGATAGTAATTTTCTACACCTTACAAATAGCTTTTAGTAT 1200
QY 1441 CGAGAGAGGATCGGTTGATCTTAACTGAATTTACCGCTTGAGGATTAATAGTGTGCA 1500
DB 1201 CGAGAGAGGATCGGTTGATCTTAACTGAATTTACCGCTTGAGGATTAATAGTGTGCA 1260
QY 1501 CCTCCGAGAGATATAGTCACTGTTTATGTCGAATTTGTTTCAAGATCTGGAACA 1560
DB 1261 CCTCCGAGAGATATAGTCACTGTTTATGTCGAATTTGTTTCAAGATCTGGAACA 1320
QY 1561 CTTTTTAAACAATCGTGTAGTATTTTCTTGGACCGATCTGAGTGAATCTTACAAAT 1620
DB 1321 CTTTTTAAACAATCGTGTAGTATTTTCTTGGACCGATCTGAGTGAATCTTACAAAT 1380
QY 1621 ACAATGTATCGAGAGAAATTAATCAATACCTTTTGTGAAAGATTTAGATTTGGGG 1680

Db 1381 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAAGATTAGAGTTTGGGGG 1440
Qy 1681 GGCACCTCTCTCAATTACAGACACAGGATTTACAGGAGGGATATCCTTCGAAGAAATACC 1740
Db 1441 GGCACCTCTCTCAATTACAGACACAGGATTTACAGGAGGGATATCCTTCGAAGAAATACC 1500
Qy 1741 TTTGGTGATTTTGTATCTCTACAGTCAATTAATTAATTCACCAATTAATCCCAAGATACCGT 1800
Db 1501 TTTGGTGATTTTGTATCTCTACAGTCAATTAATTAATTCACCAATTAATCCCAAGATACCGT 1560
Qy 1801 TTAAGATTTCTGTTACGCTTCAGTAGGATGACAGCAGTTATAGTATTAATTAACAGAGCGGCA 1860
Db 1561 TTAAGATTTCTGTTACGCTTCAGTAGGATGACAGCAGTTATAGTATTAATTAACAGAGCGGCA 1620
Qy 1861 TCCACAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA 1920
Db 1621 TCCACAGAGTGGGAGGCCAAGTTAGTGTAAATATGCTCTTCAGAAAACTATGGAATA 1680
Qy 1921 GGGAGAGTAACTAGACATAGAACATTTAGATATACCGATTTTATAGTATCCTTTTCAATTT 1980
Db 1681 GGGAGAGTAACTAGACATAGAACATTTAGATATACCGATTTTATAGTATCCTTTTCAATTT 1740
Qy 1981 AGAGCTAATCCAGATATAATTTGGATAAGTGAACACCTCTATTTGTCGAGGTTCTATT 2040
Db 1741 AGAGCTAATCCAGATATAATTTGGATAAGTGAACACCTCTATTTGTCGAGGTTCTATT 1800
Qy 2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATCTACAGATGCAACATTTGAA 2100
Db 1801 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATCTACAGATGCAACATTTGAA 1860
Qy 2101 GCAGATCTGATTTAGAAAGAGCACAAAGCGCGTGAATGCCCTGTTTACTTCTTCCAAT 2160
Db 1861 GCAGATCTGATTTAGAAAGAGCACAAAGCGCGTGAATGCCCTGTTTACTTCTTCCAAT 1920
Qy 2161 CAAATCGGTTAAAAACCGATGACGGATTAATATATGATCAAGTATCCATTTAGTG 2220
Db 1921 CAAATCGGTTAAAAACCGATGACGGATTAATATATGATCAAGTATCCATTTAGTG 1980
Qy 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGCCGAGAAAGTCAAA 2280
Db 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGCCGAGAAAGTCAAA 2040
Qy 2281 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATGCAAACTTCAGAGGATC 2340
Db 2041 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATGCAAACTTCAGAGGATC 2100
Qy 2341 AATAGACAAACGACCGTGGCTGGAGGAGTACAGATATTAACCAATCCAAAGGAGAT 2400
Db 2101 AATAGACAAACGACCGTGGCTGGAGGAGTACAGATATTAACCAATCCAAAGGAGAT 2160
Qy 2401 GAGCTATTCAAAGAGAAATACGTACACTACCGGTTACCGTTGATGAGTGCTATCCAAG 2460
Db 2161 GAGCTATTCAAAGAGAAATACGTACACTACCGGTTACCGTTGATGAGTGCTATCCAAG 2220
Qy 2461 TATTATATCAGAAATAGATGAGTGGAAATTAAGAGCTTATACCCGTTATGAATTAAGA 2520
Db 2221 TATTATATCAGAAATAGATGAGTGGAAATTAAGAGCTTATACCCGTTATGAATTAAGA 2280
Qy 2521 GGGTATATCGAGATAGTCAAGCTTAGAAATCTATTGATCGCGTACAGATGCAAAACAC 2580
Db 2281 GGGTATATCGAGATAGTCAAGCTTAGAAATCTATTGATCGGTTTACCAATGCAAAACAC 2340
Qy 2581 GAAATAGTAAATGTGCGAGCAGCGGTTCTCTTATGCGCGCTTTCAGCCCAAAAGTCCAATC 2640
Db 2341 GAAATAGTAAATGTGCGAGCAGCGGTTCTTATGCGCGCTTTCAGCCCAAAAGTCCAATC 2400
Qy 2641 GGAAAGTGGAGAACCGAATGATGCGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
Db 2401 GGAAAGTGGAGAACCGAATGATGCGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2460
Qy 2701 TGTCTCTGCAG 2711
Db 2461 TGTCTCTGCAG 2471

RESULT 6

US-09-972-175-9
; Sequence 9, Application US/0972175
; Publication No. US20030101482A1

; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light

; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

; NUMBER OF SEQUENCES: 76

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/972,175

; FILING DATE: 05-Oct-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/337,635

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: MECO:206

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512/418-3000

; TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3567 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..3567

; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-972-175-9

Query Match 89.6%; Score 2427.8; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2444; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Qy 241 ATGGAGGAGAAATAATCAAAATCAATGACATACCTTCAATTTGTTAGTAAATCCTGAAGAA 300
Db 1 ATGGAGGAGAAATAATCAAAATCAATGACATACCTTCAATTTGTTAGTAAATCCTGAAGAA 60
Qy 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATTTGATATTTCTCTGTCA 360
Db 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATTTGATATTTCTCTGTCA 120
Qy 361 CTGTGTTCAAGTTCTGATATCAATTTGTACAGGGGAGGATTTTAGTTGGATTAATA 420
Db 121 CTGTGTTCAAGTTCTGATATCAATTTGTACAGGGGAGGATTTTAGTTGGATTAATA 180
Qy 421 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 480
Db 181 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 240
Qy 481 CAATTAATTAATGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 540
|||||

Db	241	CAATTAATTAATGAAGAATAGCTGAATTTGCTAGAGATGCTGCTATTGCTTAATTAGAA	300	Qy	1621	ACAAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTAGAGTTTGGGG	1680
Qy	541	GGATTAGGAAACAAATTTCAATATATATGTGGAGCAATTTAAAGAAATGGGAGAGATCCT	600	Db	1381	ACAAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTAGAGTTTGGGG	1440
Db	301	GGATTAGGAAACAAATTTCAATATATATGTGGAGCAATTTAAAGAAATGGGAGAGATCCT	360	Qy	1681	GGCACTCTGTGTCATTAACAGAGACAGGATTTACAGGAGGGGATATCCCTTCGAAGAAATACC	1740
Qy	601	AATAATCCAGCAACACGAGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGGCTACTT	660	Db	1441	GGCACTCTGTGTCATTAACAGAGACAGGATTTACAGGAGGGGATATCCCTTCGAAGAAATACC	1500
Db	361	AATAATCCAGCAACACGAGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGGCTACTT	420	Qy	1741	TTTGGTGATTTTGTATCTCTACAGTCAATTAATTAATTTACCAATTTACCCAAAGATACCGT	1800
Qy	661	GAAGGGACATTTCTCGTTTCGAAATTTCTGGATTTTGAAGTACCCCTTTTATCCGTTTAT	720	Db	1501	TTTGGTGATTTTGTATCTCTACAGTCAATTAATTAATTTACCAATTTACCCAAAGATACCGT	1560
Db	421	GAAGGGACATTTCTCGTTTCGAAATTTCTGGATTTTGAAGTACCCCTTTTATCCGTTTAT	480	Qy	1801	TTAAGATTTTCGTTTACGCTTCCAGTAGGAGTGCAGCTAGTTATATAGTATTAACAGAGCGGCA	1860
Qy	721	GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAAATTTTGGAGAAAGA	780	Db	1561	TTAAGATTTTCGTTTACGCTTCCAGTAGGAGTGCAGCTAGTTATATAGTATTAACAGAGCGGCA	1620
Db	481	GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAAATTTTGGAGAAAGA	540	Qy	1861	TCCACAGGAGTGGGAGGCCAAAGTTAGTGTAGATAATGCTCTTTCAGAAAACTATGGAAATA	1920
Qy	781	TTTGGGATTTGACACGATAAATGTCAATGAAACCTAATAATAGACTAAATAGGCATATTCAT	840	Db	1621	TCCACAGGAGTGGGAGGCCAAAGTTAGTGTAAATATGCTCTTTCAGAAAACTATGGAAATA	1680
Db	541	TGGGATTTGACACGATAAATGTCAATGAAACCTAATAATAGACTAAATAGGCATATTCAT	600	Qy	1921	GGGGAGAACTTAAACATCTAGAAACATTTAGATATATACCGAATTTTAGTAAATCCCTTTTCAATTT	1980
Qy	841	GAAATGCTGATCAGCTGCTCAATACGATTAATTCGGGATTAATTAATTTTACCGAAATCT	900	Db	1681	GGGGAGAACTTAAACATCTAGAAACATTTAGATATATACCGAATTTTAGTAAATCCCTTTTCAATTT	1740
Db	601	GAAATGCTGATCAGCTGCTCAATACGATTAATTCGGGATTAATTAATTTTACCGAAATCT	660	Qy	1981	AGAGCTTAATCCAGATATAAATTTGGGATAAGTGAACCAACCTCTATTTTGGTGCAGGTTCTATT	2040
Qy	901	AGATATCAAGATTTGGATTAACATATTAATCGATTACGAGAGACTTAAACATTTAGCTGATTA	960	Db	1741	AGAGCTTAATCCAGATATAAATTTGGGATAAGTGAACCAACCTCTATTTTGGTGCAGGTTCTATT	1800
Db	661	AGATATCAAGATTTGGATTAACATATTAATCGATTACGAGAGACTTAAACATTTAGCTGATTA	720	Qy	2041	AGTAGCGTGTGAACCTTTATATAGATTAATTAATTAATTTCTAGCAGATGCAACATTTGAA	2100
Qy	961	GATATCGCGCTTTCTTTTCCAACTATGACAAATAGAGATTCOAATTCAGCGAGTTGGT	1020	Db	1801	AGTAGCGTGTGAACCTTTATATAGATTAATTAATTTGAAATTTATTTAGCAGATGCAACATTTGAA	1860
Db	721	GATATCGCGCTTTCTTTTCCAACTATGACAAATAGAGATTCOAATTCAGCGAGTTGGT	780	Qy	2101	GCAGAAATCTGATTTAGAAAGACCAAAAAGCGGTGAAATGCCCTGTTTACTTCTTCCCAAT	2160
Qy	1021	CAACTAAACAAGGGAAGTTTATACGGAACCAATTAATTAATTTTAACTCCACAGTTPACAGTCT	1080	Db	1861	GCAGAAATCTGATTTAGAAAGACCAAAAAGCGGTGAAATGCCCTGTTTACTTCTTCCCAAT	1920
Db	781	CAACTAAACAAGGGAAGTTTATACGGAACCAATTAATTAATTTTAACTCCACAGTTPACAGTCT	840	Qy	2161	CAAAATCGGGTTAAAAACCGATGTGACGGATATCATATTTGATCAAGTATCCAAATTTAGTG	2220
Qy	1081	GTAGCTTCAATTAACCTTTTAACTGTTATAGAGAGCAGCGCAATTTAGAAATCCCTCAATTA	1140	Db	1921	CNAATCGGGTTAAAAACCGATGTGACGGATATCATATTTGATCAAGTATCCAAATTTAGTG	1980
Db	841	GTAGCTTCAATTAACCTTTTAACTGTTATAGAGAGCAGCGCAATTTAGAAATCCCTCAATTA	900	Qy	2221	GATTTGTTTATCAGATGAAATTTTGTCTGGATGAAAGCGAGAAATTTCTCGCAGAGAAAGTCAAA	2280
Qy	1141	TTTGTATATTAATTAATCTTTACAACTTTTACGGATTTGTTTGTGTTGAGCAGCAATTTT	1200	Db	1981	GATTTGTTTATCAGATGAAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAAAGTCAAA	2040
Db	901	TTTGTATATTAATTAATCTTTACAACTTTTACGGATTTGTTTGTGTTGAGCAGCAATTTT	960	Qy	2281	CATTCGGAACCGACTCAGTGTGATGAGCGGAAATTTACTTCAAGATCCAAACCTTCAGAGGATC	2340
Qy	1201	TATTTGGGAGGACATCCAGTATATATCTAGCTTATAGGAGTGGTAACTAAACATCTCTCT	1260	Db	2041	CATTCGGAACCGACTCAGTGTGATGAGCGGAAATTTACTTCAAGATCCAAACCTTCAGAGGATC	2100
Db	961	TATTTGGGAGGACATCCAGTATATATCTAGCTTATAGGAGTGGTAACTAAACATCTCTCT	1020	Qy	2341	AAATAGAACACAGACCGTGTGCTGGAGAGGAAATACAGATATACCATCAAGAGGAGGAT	2400
Qy	1261	ATATATGAGAGAGGCGAACGAGGCGCTCCAGATTCCTTTACTTTTATGAGCGGTA	1320	Db	2101	AAATAGAACACAGACCGTGTGCTGGAGAGGAAATACAGATATACCATCAAGAGGAGGAT	2160
Db	1021	ATATATGAGAGAGGCGAACGAGGCGCTCCAGATTCCTTTACTTTTATGAGCGGTA	1080	Qy	2401	GAGTATTCAAAAGAGAAATACGTACACCTTACCGGTACCGTTGATGAGTGTCTATCCAAAG	2460
Qy	1321	TTTAGGACTTTATCAAAATCTCTTTACGATTAATACAGCAACCTTCGAGCGCAACAT	1380	Db	2161	GAGTATTCAAAAGAGAAATACGTACACCTTACCGGTACCGTTGATGAGTGTCTATCCAAAG	2220
Db	1081	TTTAGGACTTTATCAAAATCTCTTTACGATTAATACAGCAACCTTCGAGCGCAACAT	1140	Qy	2461	TATTTATATCAGAAATAGATGATCGAAATTTAAAGCTTTTATACCGTTTATGAATTAAGA	2520
Qy	1381	TTTAAATTTACGTTGGTGAAGAGTAGAATTTTCTACCTTACAAATAGCTTTAGTAT	1440	Db	2221	TATTTATATCAGAAATAGATGATCGAAATTTAAAGCTTTTATACCGTTTATGAATTAAGA	2280
Db	1141	TTTAAATTTACGTTGGTGAAGAGTAGAATTTTCTACCTTACAAATAGCTTTTAGTAT	1200	Qy	2521	GGGTATTCGAGATAGTCTAAGACTTTAGAAATCTTTGATCGGTGACCTCAAGTCAACAC	2580
Qy	1441	GCAGGAAGAGGTACGGTTGATTTCTTAACTGAAATACCGCTGAGGATTAATAGTGTGCA	1500	Db	2281	GGGTATTCGAGATAGTCTAAGACTTTAGAAATCTTTGATCGGTGACCTCAAGTCAACAC	2340
Db	1201	CGAGGAAGAGGTACGGTTGATTTCTTAACTGAAATACCGCTGAGGATTAATAG					

QY 2701 TGTTCCTGCAG 2711
DB 2461 TGTTCCTGCAG 2471

RESULT 7

US-09-972-175-7

; Sequence 7, Application US/09972175

; Publication No. US20030101482A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; Gilmer, Amy Jelen

; Metcus, Anne-Marie Light

; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING

; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

; NUMBER OF SEQUENCES: 76

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION NUMBER: US/09/972,175

; FILING DATE: 05-Oct-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/337,635

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: MECO:206

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512/418-3000

; TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3567 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..3567

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-972-175-7

Query Match 89.5%; Score 2426.2; DB 11; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2443; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATAATCAAAATCAATGCATACCTTACCAATGTTTAAAGTAATCCTGAAGAA 300
DB 1 ATGGAGGAAATAATCAAAATCAATGCATACCTTACCAATGTTTAAAGTAATCCTGAAGAA 60
QY 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATGATATTTCTGTGCA 360
DB 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATGATATTTCTGTGCA 120
QY 361 CTGTGTCAGTTTCTGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGGATTAATA 420
DB 121 CTGTGTCAGTTTCTGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGGATTAATA 180
QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
DB 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240

QY 481 CAATTAATTAATGAAAGAAATAGCTGAAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 540
DB 241 CAATTAATTAATGAAAGAAATAGCTGAAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 300
QY 541 GGATTAGGAAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGAATCCT 600
DB 301 GGATTAGGAAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGAATCCT 360
QY 601 AATAATCCAGCAACCCAGGACAGAGTAATTTGATCGCTTTTCGTTATCTTCTGATCGGCTACT 660
DB 361 CATATCCCAACCAACGAGGACAGAGTAATTTGATCGCTTTTCGTTATCTTCTGATCGGCTACT 420
QY 661 GAAAGGACATTTCTTTTCGTTTCGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTAT 720
DB 421 GAAAGGACATTTCTTTTCGTTTCGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTAT 480
QY 721 GCTCAAGCGGCAATCTGCACTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGA 780
DB 481 GCTCAAGCGGCAATCTGCACTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGA 540
QY 781 TTGGGATTTGACAAACGATAAATGCTCAATGAAAACTATATAGACTAATTAGGATATTGAT 840
DB 541 TGGGGATTTGACAAACGATAAATGCTCAATGAAAACTATATAGACTAATTAGGATATTGAT 600
QY 841 GAATATGCTGATCACTGTGCAAAATACGTATATATCGGGATTTAAATAATTTACCGAAATCT 900
DB 601 GAATATGCTGATCACTGTGCAAAATACGTATATATCGGGATTTAAATAATTTACCGAAATCT 660
QY 901 ACGTATCAAGATTTGGATAACATATATCGATTCGAGAGAGACTTAACATTTGATTTA 960
DB 661 ACGTATCAAGATTTGGATAACATATATCGATTCGAGAGAGACTTAACATTTGATTTA 720
QY 961 GATATCGCGCTTTCTTTCCAAACTATGACATAGAGATATCCAAATTCAGGACGTTGGT 1020
DB 721 GATATCGCGCTTTCTTTCCAAACTATGACATAGAGATATCCAAATTCAGGACGTTGGT 780
QY 1021 CAATTAACAAAGGAAAGTTTATACGGACCAATTAATTTTAAATTTTAAATCCACAGTTTACAGTCT 1080
DB 781 CAATTAACAAAGGAAAGTTTATACGGACCAATTAATTTTAAATTTTAAATCCACAGTTTACAGTCT 840
QY 1081 GTAGCTCAATTTACCTTAACTTTTAACTTTGAGAGAGAGCGCAATTTAGAAATCCTCATTTA 1140
DB 841 GTAGCTCAATTTACCTTAACTTTTAACTTTGAGAGAGAGCGCAATTTAGAAATCCTCATTTA 900
QY 1141 TTTGATATTTGAATAATCTTACCAATCTTTACGGATTTGTTAGTTGGAGCAATTTT 1200
DB 901 TTTGATATTTGAATAATCTTACCAATCTTTACGGATTTGTTAGTTGGAGCAATTTT 960
QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGTGGTAAACATATACATCTCCT 1260
DB 961 TATTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGTGGTAAACATATACATCTCCT 1020
QY 1261 ATATATGGAAGAGAGCGGAAACAGGAGGCTTCAAGATCTTTTACCTTTTAAATGGACGGTA 1320
DB 1021 ATATATGGAAGAGAGCGGAAACAGGAGGCTTCAAGATCTTTTACCTTTTAAATGGACGGTA 1080
QY 1321 TTTAGGACTTTTATCAATTTCTTACGATTTATACGACACCTTGGCAGCGCCACCAT 1380
DB 1081 TTTAGGACTTTTATCAATTTCTTACGATTTATACGACACCTTGGCAGCGCCACCAT 1140
QY 1381 TTTAATTTTACGTTGGTGGAGGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTAAT 1440
DB 1141 TTTAATTTTACGTTGGTGGAGGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTAAT 1200
QY 1441 CGAGGAAGAGGTACGGTTGATTTCTTAACTGAATTTACCGCTTGAGGATAATAGTGTGCA 1500
DB 1201 CGAGGAAGAGGTACGGTTGATTTCTTAACTGAATTTACCGCTTGAGGATAATAGTGTGCA 1260
QY 1501 CCTCGGAGGATATAGTCATGCTTTTATGTCATGCAACTTTTGTTCGAAAGATCTGGAACA 1560
DB 1261 CCTCGGAGGATATAGTCATGCTTTTATGTCATGCAACTTTTGTTCGAAAGATCTGGAACA 1320

QY 1561 CCTTTTAAACAACTGGTGTAGTATTTCTTGGAGCGCATCGTAGTCAACTCTTACAAAT 1620
Db 1321 CCTTTTAAACAACTGGTGTAGTATTTCTTGGAGCGCATCGTAGTCAACTCTTACAAAT 1380
QY 1621 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTGGGGG 1680
Db 1381 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTGGGGG 1440
QY 1681 GGCACCTCTGTCAATTACAGGACAGGATTTACAGAGGGGATATCTCTCGAAGAAATACC 1740
Db 1441 GGCACCTCTGTCAATTACAGGACAGGATTTACAGAGGGGATATCTCTCGAAGAAATACC 1500
QY 1741 TTTGGTGATTTTGTATCTCTACAGTCAATATTAATCACCAGTATACCCAAAGATACCGT 1800
Db 1501 TTTGGTGATTTTGTATCTCTACAGTCAATATTAATCACCAGTATACCCAAAGATACCGT 1560
QY 1801 TTAAGATTTTCGTTAGCTTCCAGTAGGGATGACAGTATAGTATTAACAGAGCGGCA 1860
Db 1561 TTAAGATTTTCGTTAGCTTCCAGTAGGGATGACAGTATAGTATTAACAGAGCGGCA 1620
QY 1861 TCCACAGGATGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA 1920
Db 1621 TCCACAGGATGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTATCTCTTTTCATTT 1980
Db 1681 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTATCTCTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATATTTGGGATAAGTGAACAACTCTATTTGGTCAGGTTCTATT 2040
Db 1741 AGAGCTAATCCAGATATATTTGGGATAAGTGAACAACTCTATTTGGTCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTTCTAGCAGATCAACATTTGAA 2100
Db 1801 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTTCTAGCAGATCAACATTTGAA 1860
QY 2101 GCAGATCTGATTTAGAAAGAGACAAAAGGCGGTGAATGCCCTGTTACTTCTTCCAAT 2160
Db 1861 GCAGATCTGATTTAGAAAGAGACAAAAGGCGGTGAATGCCCTGTTACTTCTTCCAAT 1920
QY 2161 CAATCGGTTTAAACCCGATGTCGAGGATATCATATTTGATCAAGTATCCATTTAGTG 2220
Db 1921 CAATCGGTTTAAACCCGATGTCGAGGATATCATATTTGATCAAGTATCCATTTAGTG 1980
QY 2221 GATTTGTTATCAGATCAATTTGTCGATGAAGAGGAGATTTGCGAGAACTGAAA 2280
Db 1981 GATTTGTTATCAGATCAATTTGTCGATGAAGAGGAGATTTGCGAGAACTGAAA 2040
QY 2281 CATGCGAAGGACTCAGTGTAGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2340
Db 2041 CATGCGAAGGACTCAGTGTAGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2100
QY 2341 AATAGACAAACCGACCGTGGCTGGAGGAGATACAGATATTTACCATCCAAAGGAGAGAT 2400
Db 2101 AATAGACAAACCGACCGTGGCTGGAGGAGATACAGATATTTACCATCCAAAGGAGAGAT 2160
QY 2401 GAGCTATCCAAAGAGAAATACGTCACACTACCGGTCGCTTGATGAGTGTATCCAAAG 2460
Db 2161 GAGCTATCCAAAGAGAAATACGTCACACTACCGGTCGCTTGATGAGTGTATCCAAAG 2220
QY 2461 TATTTATACAGAAATAGATGAGTCGAATTTAAAGCTTATACCCGTTATCAATTAAGA 2520
Db 2221 TATTTATACAGAAATAGATGAGTCGAATTTAAAGCTTATACCCGTTATCAATTAAGA 2280
QY 2521 GGGTATATCGAAGATAGTCAGACTTAGAATCTATTTGATCGGTCAGATCAAAACAC 2580
Db 2281 GGGTATATCGAAGATAGTCAGACTTAGAATCTATTTGATCGGTCAGATCAAAACAC 2340
QY 2581 GAATATGATTAATTCGAGGACGAGTCTTATCTTATGCTTTCAGCCCAAGATCCAAATC 2640
Db 2341 GAATATGATTAATTCGAGGACGAGTCTTATGCTTTCAGCCCAAGATCCAAATC 2400
QY 2641 GGAAAGTGTGGAGAACCGAATCGATGCGGCCACACACTTGTGAATGGATCTGTAGT 2700

Db 2401 GGAAAGTGTGGAGAACCGAATCGATGCGGCCACACCTTGAATGGATCTGTAGT 2460
QY 2701 TGTTCCTGCAG 2711
Db 2461 TGTTCCTGCAG 2471
RESULT 8
US-09-972-175-58
; Sequence 58, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-2577
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-972-175-58
Query Match 89.3%; Score 2419.8; DB 11; Length 3567;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2439; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 241 ATGAGGAGAAATTAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAA 300
Db 1 ATGAGGAGAAATTAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAA 60
QY 301 GTACTTTTGGATGGAGACGGATATCAACTGGTAATTAATCTCAATTTGATATTTCTCTGTCA 360
Db 61 GTACTTTTGGATGGAGACGGATATCAACTGGTAATTAATCTCAATTTGATATTTCTCTGTCA 120
QY 361 CTTCTTCAGTTCTGTTCTTAATCTTAACTTTGTACACGGGGAGGATTTTGTAGTTGGATTAATA 420
Db 121 CTTCTTCAGTTCTGTTCTTAATCTTAACTTTGTACACGGGGAGGATTTTGTAGTTGGATTAATA 180

[illegible]

Db 1201 CGAGGAGAGGTACGGTTCATCTTTAACTGAATTAACCCCTGAGGATTAATAGTGTGCCA 1260
Qy 1501 CCTCGGAAGGATATAGTTCATCGTTTATGTATGTCACAACTTTTGTTCAAAGATCTGGAA 1560
Db 1261 CCTCGGAAGGATATAGTTCATCGTTTATGTATGTCACAACTTTTGTTCAAAGATCTGGAA 1320
Qy 1561 CCTTTTAACTCGGTGTAGTATTTTCTTGACGATCGTAGTGCACACTCTTCAAAAT 1620
Db 1321 CCTTTTAACTCGGTGTAGTATTTTCTTGACGATCGTAGTGCACACTCTTCAAAAT 1380
Qy 1621 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTGGGG 1680
Db 1381 ACAATTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTGGGG 1440
Qy 1681 GGCACCTCTGTCAATACAGGACAGGATTAACAGGAGGGATATCCTTCGAAGAAATACC 1740
Db 1441 GGCACCTCTGTCAATACAGGACAGGATTAACAGGAGGGATATCCTTCGAAGAAATACC 1500
Qy 1741 TTTGGTGAATTTGTATCTCTACAGTCAATATTAATTAACCAATTAACCAAGATACCGT 1800
Db 1501 TTTGGTGAATTTGTATCTCTACAGTCAATATTAATTAACCAATTAACCAAGATACCGT 1560
Qy 1801 TTAAGATTTTCTAGCTTCCAGTAGGGATGACAGTATATAGTATTAACAGAGCGCA 1860
Db 1561 TTAAGATTTTCTAGCTTCCAGTAGGGATGACAGTATATAGTATTAACAGAGCGCA 1620
Qy 1861 TCCACAGGAGTGGGAGCCCAAGTTAGTGTAGATATGCTCTTTCAGAAACTATGGAATA 1920
Db 1621 TCCACAGGAGTGGGAGCCCAAGTTAGTGTAAATATGCTCTTTCAGAAACTATGGAATA 1680
Qy 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTAATCTTTTCAATTT 1980
Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTAATCTTTTCAATTT 1740
Qy 1981 AGAGCTTAATCCAGATATATGCGATAAGTGAACACCTCTATTTGGTGCAGGTTCTATT 2040
Db 1741 AGAGCTTAATCCAGATATATGCGATAAGTGAACACCTCTATTTGGTGCAGGTTCTATT 1800
Qy 2041 AGTAGCGTTGAATTTATATAGATAAAATTTGAAATTTATCTAGCAGATCAACATTTGAA 2100
Db 1801 AGTAGCGTTGAATTTATATAGATAAAATTTGAAATTTATCTAGCAGATCAACATTTGAA 1860
Qy 2101 CGAGAACTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTACTTCTTCCAAT 2160
Db 1861 CGAGAACTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTACTTCTTCCAAT 1920
Qy 2161 CAAATCGGTTTAAACCCGATCTGAGGATATCATATTTGATCAAGTATCCAAATTTAGT 2220
Db 1921 CAAATCGGTTTAAACCCGATCTGAGGATATCATATTTGATCAAGTATCCAAATTTAGT 1980
Qy 2221 GATTTGTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGCGAGAAAGTCAAA 2280
Db 1981 GATTTGTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGCGAGAAAGTCAAA 2040
Qy 2281 CATGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATC 2340
Db 2041 CATGGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATC 2100
Qy 2341 AATAGACACACGCGTGGCTGGAGAGGAATTAATTTCAAGATCCAAACTTCAGAGGATC 2400
Db 2101 AATAGACACACGCGTGGCTGGAGAGGAATTAATTTCAAGATCCAAACTTCAGAGGATC 2160
Qy 2401 GACGTATTCAAAGAGAAATTAACGTCACTACCGGTACCGTTGATGAGTCTATCCAAG 2460
Db 2161 GACGTATTCAAAGAGAAATTAACGTCACTACCGGTACCGTTGATGAGTCTATCCAAG 2220
Qy 2461 TATTTATATCAGAAATAGATGAGTCAAGATTTAAAGCTTATACCGGTTATGAATTAAGA 2520
Db 2221 TATTTATATCAGAAATAGATGAGTCAAGATTTAAAGCTTATACCGGTTATGAATTAAGA 2280
Qy 2521 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTTGATCGGTACATGCAAAACAC 2580
Db 2281 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTTGATCGGTATCAATTCAAACAC 2340

Qy 2581 GAAATAGTAAATGTGCCAGGCAAGGTTCTTTATGCGCGCTTTTACGCCAAAGTCCAATC 2640
Db 2341 GAAATAGTAAATGTGCCAGGCAAGGTTCTTTATGCGCGCTTTTACGCCAAAGTCCAATC 2400
Qy 2641 GGAAGTGTGGAGAACCAATCGATGCGGCCACACCTTGAATGGAATCTGATCTAGAT 2700
Db 2401 GGAAGTGTGGAGAACCAATCGATGCGGCCACACCTTGAATGGAATCTGATCTAGAT 2460
Qy 2701 TGTTCCTGCAG 2711
Db 2461 TGTTCCTGCAG 2471

RESULT 10

US-09-826-660-20
; Sequence 20, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-20

Query Match 63.9%; Score 1733.2; DB 9; Length 3489;
Best Local Similarity 82.4%; Pred. No. 0;
Matches 1987; Conservative 0; Mismatches 423; Indels 0; Gaps 0;

Qy 241 ATGGAGGAAATTAATCAAAATCAATGATACCTTCAATTTGTTAAGTAATCTCGAAGNA 300
Db 1 ATGGAGGAGAACAAATCAGAAATCAGTGCATACCTTCAAACTGCTTGAGCAATCTGAAGAG 60
Qy 301 GTACTTTTGGATGGAGAACGGATATCAACTGCTAATTAATCAATGATATTTCTCTGTCA 360
Db 61 GTACTTCTTGATGGAGAACGGATCTCAACTGCTGTAATCTTAGCATTTGACATCTCACTGCA 120
Qy 361 CTGTGTCAGTTTCTGATATCTAACTTTGTACAGGGGAGGATTTTGTAGTTGGAATTAATA 420
Db 121 CTGTGTCAGTTTCTGATCTCAACTTTGTTCCAGGGGTGGCTTTCTTGTGGAATCTATA 180
Qy 421 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
Db 181 GACTTTGTGTGGGCAATTTGTTGGCCCATCTCAATGGGATGCTTCTTGTGACAGATTGAA 240
Qy 481 CAAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTTAGTAAATAGAA 540
Db 241 CAGTTGATCAATGAGAGGATAGCTGAGTTTGTAGGAATGCTGCCAATTTGCCAATCTGAA 300
Qy 541 GGATTTAGGAACAATTTCAATATATATGTTGAAGCATTTAAAGAAATGGGAAGATCCT 600
Db 301 GGATTTAGGAACAATTTCAATATATATGTTGAAGCATTTCAAGAAATGGGAAGATCCC 360
Qy 601 AATTAATCAGCAACAGAGACAGAGTAATTAATGCTTTTGTATGATGCTGATGCGGTACTTT 660
Db 361 AACATCCAGCAACCCGTAACGAGAGTCAATGATGCTTTTGGATACCTTTGATGGGCTACTT 420

QY 661 GAAAGGACATTCCTCGTTTCGAAATTTCTCGAATTTGAAGTACCCCTTTTATCGTTTAT 720
Db 421 GAAAGGACATTCCTCGTTTCGAAATTTCTCGAATTTGAAGTACCCCTTTTATCGTTTAT 480
QY 721 GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGAGANTCTGTAAATTTTGGAGAAAGA 780
Db 481 GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGAGANTCTGTGTGATCTTTGGAGAAAGA 540
QY 781 TTGGGATTCGACAAATGATTAATGATAAATGATAAATGATAAATGATAAATGATAAATGATA 840
Db 541 TTGGGATTCGACAAATGATTAATGATAAATGATAAATGATAAATGATAAATGATAAATGATA 600
QY 841 GAATATGCTGATCACTGTGCAATACGTAATACGTAATACGTAATACGTAATACGTAATACG 900
Db 601 GAGTATGCTGATCACTGTGCAATACGTAATACGTAATACGTAATACGTAATACGTAATACG 660
QY 901 ACCTATCAAGATTCGATTAATCAATATCGATTACGAGAGACTTTAACTTGAATGATTA 960
Db 661 ACCTATCAAGATTCGATTAATCAATATCGATTACGAGAGACTTTAACTTGAATGATTA 720
QY 961 GATATCGGCTTCTTTCGAACTATGATATGATATGATATGATATGATATGATATGATATGAT 1020
Db 721 GATATCGGCTTCTTTCGAACTATGATATGATATGATATGATATGATATGATATGATATGAT 780
QY 1021 CAATTAACAGGGAATTTATACGACCCATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
Db 781 CAATTAACAGGGAATTTATACGACCCATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 1081 GTAGTCAATTAACGATTTTAACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 841 GTTCTCAGTTACCTACTTCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 1141 TTTGATATATTAATTAATTTAACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 901 TTTGATATATTAATTAATTTAACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 1201 TATTTGGGAGAGACATCGAGTAAATCTAGCTTTATAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 961 TACTGGGAGAGACATCGAGTAAATCTAGCTTTATAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1261 ATATATGGAAG 1320
Db 1021 ATCTATGTTAGGAG 1080
QY 1321 TTTAGGACTTTTATCAATTTCTACTTTAGGATTTATAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1081 TTTAGGACTTTTATCAATTTCTACTTTAGGATTTATAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1381 TTTTATTTAGGAG 1440
Db 1141 TTTCAATTTAGGAG 1200
QY 1441 GCAGGAG 1500
Db 1201 CGTGGAG 1260
QY 1501 CTTGGGAG 1560
Db 1261 CTTGGGAG 1320
QY 1561 CTTTATTAACAACTGTGTAGATTTTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1321 CCGTTCCTGACAACTGTGTAGATTTTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1621 ACAATTTGATTCAG 1680
Db 1381 ACAATTTGATTCAG 1440
QY 1681 GGCACCTCTGTCTATTTACAGGAG 1740
Db 1441 GGCACCTCTGTCTATTTACAGGAG 1500

QY 1741 TTTGGTATTTTGTATCTCTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
Db 1501 TTTGGTATTTTGTATCTCTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
QY 1801 TTAAGATTTTGGTTTACGCTTCCAGTAGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1561 CTAAGTTTTCGTTTACGCTTCCAGTAGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1861 TCCACAG 1920
Db 1621 TCCACAG 1680
QY 1921 GGGGAG 1980
Db 1681 GGGGAG 1740
QY 1981 AGAGCTATCCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
Db 1741 AGAGCTATCCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
QY 2041 AGTACGCTTGAATTTTATATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2100
Db 1801 AGTACGCTTGAATTTTATATAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
QY 2101 GCAGAAATCTGATTTTGAAG 2160
Db 1861 GCAGAAATCTGATTTTGAAG 1920
QY 2161 CAAATCGGCTTAAAAACCGATGAG 2220
Db 1921 CAAATCGGCTTAAAAACCGATGAG 1980
QY 2221 GATTTGTTATCAGATTAATTTTGTCTGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Db 1981 GATTTGTTATCAGATTAATTTTGTCTGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
QY 2281 CATGTAACCGGACTTAGTGTAGATGAGCGGAAATTTTCTTCAAGATCCAAATTTTTCGCGGGGATC 2340
Db 2041 CATGTAACCGGACTTAGTGTAGATGAGCGGAAATTTTCTTCAAGATCCAAATTTTTCGCGGGGATC 2100
QY 2341 AATAGAGAACCGAG 2400
Db 2101 AACAGGCACTAGATCGTGGATGAG 2160
QY 2401 GAGCTATTCAG 2460
Db 2161 GAGCTATTCAG 2220
QY 2461 TATTTATATCAGAAATAGATGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2520
Db 2221 TATTTATATCAGAAATAGATGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2280
QY 2521 GGGTATTCAG 2580
Db 2281 GGGTATTCAG 2340
QY 2581 GAAATAGTAAATGTCAGGAG 2640
Db 2341 GAAATAGTAAATGTCAGGAG 2400
QY 2641 GCGAAGGTGTG 2650
Db 2401 GCGAAGGTGTG 2410

RESULT 11
US-09-873-873-29
; Sequence 29, Application US/09873873
; Patent No. US2002064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins

FILE REFERENCE: MECO:210--2
 CURRENT APPLICATION NUMBER: US/09/873, 873
 CURRENT FILING DATE: 2001-08-20
 PRIOR APPLICATION NUMBER: US 09/253,341
 PRIOR FILING DATE: 1999-02-19
 PRIOR APPLICATION NUMBER: US 08/922,505
 PRIOR FILING DATE: 1997-09-03
 PRIOR APPLICATION NUMBER: US 08/754,490
 PRIOR FILING DATE: 1996-11-20
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 29
 LENGTH: 3579
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Hybrid Delta-Endotoxin
 US-09-873-873-29

Query Match 55.3%; Score 1498.2; DB 9; Length 3579;
 Best Local Similarity 77.5%; Pred. No. 1.1e-310;
 Matches 1924; Conservative 0; Mismatches 508; Indels 51; Gaps 7;

QY	259	AATCAATGCATACCTTACAAATGTTAAAGTAACTCTCGAAGAGTACTTTTGGATGAGAA	318
DB	22	AATGAATGCATTCCTTATATATGTTTAAAGTAACTCGAAGTAAAGTATTTAGGTGGAGAA	81
QY	319	CGGATATCAACTGGTAAATTAATCTCAATTTGATATTTCTCTGTCACCTGTCAGTTCTTGTA	378
DB	82	AGAAATAGAACTGGTTACACCCCAATCGATATTTCTCTGTCGTAACGCAATTTCTTTTG	141
QY	379	TCTAATCTTTGTACAGGGGAGATTTTGTAGTTGGAATTAATAGATTTTGTATGGGAATA	438
DB	142	AGTGAATTTGTTCCCGGTGCTGATTTGTGTAGGACTAGTTGATATAATATATGGGAAAT	201
QY	439	GTTGGCCCTCTCAATGGGATGCAATTTCTAGTACAAATTTGAACAATTAATTAATGAAGA	498
DB	202	TTTGGTCCCTCTCAATGGGACGCAATTTCTGTGACAAATTTGAACAGTTAAATCAACAA	261
QY	499	ATAGCTGAATTTGCTAGGAATGCTGCTATTGCTTAATTTTAGAAGGATTTAGGAACAATTC	558
DB	262	ATAGAAGATTCGCTAGGAACCAAGCCATTTCTAGATTAAGAGGACTAAGCAATCTTTAT	321
QY	559	AATATATATGTGAAGCATTTAAAGAAATGGGAAGAGATCTTAATTAATCCAGCAACAGG	618
DB	322	CAAAATTTACGCAGAACTTTTAGAGAGTGGGAAGCAGATCTTACTTAATCCAGCATTAAGA	381
QY	619	ACCAGATTAATGATCGCTTTGCTATCTGTATCTGTAGTGGCTACTTGAAGGAGCAATTCCT	678
DB	382	GAAGAGATCGGTATTCAAATTTCAATGAACATGAACAGTGCCTTTACAAACCGCTATTCCT	441
QY	679	TTTCGAATTTCTGGATTTGAAGTACCCCTTTTATCGTTTATGCTCAAGCGGCCAATCTG	738
DB	442	TTTGCAGTTCAAAATATCAAGTCTCTTTTATCAGTATATGTTCAAGCTGCAAAATTTA	501
QY	739	CATCTAGCTATATTAAGAGATCTGTAAATTTTGGAGAAGATTTGGGATTTGACAAAGATA	798
DB	502	CATTATATCAGTTTGAAGATGTTTCAGTGTTTGGACAAAGGTGGGATTTGATGCGCGG	561
QY	799	AATGTCAATGAAGAACTAATATAGACTAATTTAGGCATATTTAGTGAATATCTGATCACTGT	858
DB	562	ACTATCAATAGTCGTTTATATGAATTTAACTAGGCTTTATTTGGCAACTATACAGATTA	621
QY	859	GCAAATACCTGATAATCGGGGATTTAAATAATTTTACCGAAATCTACGTATCAAGATTTG	918
DB	622	GTACGCTGTGACAAATACGGGATTTAGAACGTGTATGGGGACCGGATTTAGAGATTTGG	681
QY	919	ACATATAATCGATTAACGGAGAGACTTAACATTTGACTGTATTAAGATATCCCGCTTTCT	978
DB	682	AGGTATAATCAATTTTAGAAGAGATTTAACTAACTGTATTAAGATATCGTGTCTGTTTC	741
QY	979	CCAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTTGGTCAACTAAACAGGGAAT	1038

DB	742	CCGAATTTATGATAGTAGAAGATATCCAAATTCGAACAGTTTCCCAATTAACAAGAGAAAT	801
QY	1039	TATACGACCCCATTAATTAATTTTAAATCCACAGTTTACAGTCTGTAGCTCAATTTACCTACT	1098
DB	802	TATACAAACCCAGTATTAGA-----AAATTTTGATGGTAGTTTTCAGGC	846
QY	1099	TTTAACGTTATGAGAGCAGCGCAATTAGAAATCTCATTTATTTTATTTGATATATTGAATAAT	1158
DB	847	TCGGCTCAGGGCATAGAAAGAGTATTAGGAGTCCACATTTGTATGATATCTTAAACAGT	906
QY	1159	CTTACAATCTTTACCGATTTGTTAGTGTGGACGCAATTTTATTTGGGAGGACATCGA	1218
DB	907	ATAACCATCTATACGGATGCTCATAGG-----GTTATTAATTTGGTCAGGGCATCAA	960
QY	1219	GTAATATCTAGCCTTATAGG-----AGGTGGTAAACATAACATCTCTATATATGGAAGA	1272
DB	961	ATAATGGCTTCTCTGTAGGGTTTTCGGGGCCAGAAATTCACTTTCCGCTATATGGAAT	1020
QY	1273	GAGGGAACCCAGAGCCTCCAAGATCTTTTACCTTTTAA---TGGACCGGTATTTAGGACT	1329
DB	1021	ATGGGAAATGACAGTCCACAAACAGTATTTGTGCTCAACTAGGTCAAGGCGGTATAGA	1080
QY	1330	TTATCAATTCCTACTTTACGATTTATACAGCAACCTTGCAGCGGCCACCATTTTAATTTA	1389
DB	1081	ACATATATCGTCCACTTTATATAGAAAGCCTTTTAAATATAGGATATAATCAACAACTA	1140
QY	1390	CGTGTGGTGAAGAGTAGAATTTTCT-----ACACCTCAAAATAGCTTTTACG-----	1437
DB	1141	TCGTGTTCTTGACGGGACAGAAATTTGCTTATGGAACTCTCTCAATTTGGCATCCGCTGTA	1200
QY	1438	TATGAGGAAGAGTAGTGGTTCATTTTAACTGAATTAACCGCTGAGGATTAATAGTGTG	1497
DB	1201	TACAGAAAAAGCGAAGCGTAGATTCGCTGGATGAATACCGCCACAGAAATAACAACGTG	1260
QY	1498	CCACCTCGCGRAGGATATAGTCACTGTTTATGTCATGCAACTTTTGTTC-----AA	1548
DB	1261	CCACCTAGGCAAGGATTTAGTCACTCGATTAAGCCATGTTTCAATGTTTCAGGCTTT	1320
QY	1549	AGATCTGGAACACCTTTTAAACAACCTGGTGTAGTATTTCTTGGACGATCGTACTGCA	1608
DB	1321	AGTAATAGTAGTGAAGTATAATAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCA	1380
QY	1609	ACTTTTCAAAATCAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTGTGAAAGATTT	1668
DB	1381	ACTTTTCAAAATCAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTGTGAAAGATTT	1440
QY	1669	AGAGTTTGGGGGGGACCTCTCTGTCATTAACAGACAGGATTTTACAGGAGGGATATCCTT	1728
DB	1441	AGAGTTTGGGGGGGACCTCTCTGTCATTAACAGACAGGATTTTACAGGAGGGATATCCTT	1500
QY	1729	CGAAGAAATACCTTTTGGTGTATTTGTCATCTCAAGTCAATTAATTAATTCACCAATTACC	1788
DB	1501	CGAAGAAATACCTTTTGGTGTATTTGTCATCTCAAGTCAATTAATTAATTCACCAATTACC	1560
QY	1789	CAAGATACCGTTTAAAGATTTTCGTTACGCTCCAGTAGGGATGACAGCTTATAGTATTA	1848
DB	1561	CAAGATACCGTTTAAAGATTTTCGTTACGCTCCAGTAGGGATGACAGCTTATAGTATTA	1620
QY	1849	ACAGAGCGGCATCCACAGGAGTGGAGGCCAAGTTAGTGTAGATATGCTCTCTTCAAGAA	1908
DB	1621	ACAGAGCGGCATCCACAGGAGTGGAGGCCAAGTTAGTGTAGATATGCTCTCTTCAAGAA	1680
QY	1909	ACTATGGAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT	1968
DB	1681	ACTATGGAATAGGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAAT	1740
QY	1969	CTTTTTCATTTTAGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTGTGT	2028
DB	1741	CTTTTTCATTTTAGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTGTGT	1800
QY	2029	GCAGTTCTTATAGTGGGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGAT	2088
DB	1801	GCAGTTCTTATAGTGGGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGAT	1860

		Matches 1924; Conservative 0; Mismatches 508; Indels 51; Gaps 7;	
QY	259	ATCAATGCAATCTTCAATTTAGTAAAGAGAGCAAAAGCGCGTGAATGCTGTTT	2148
DB	1861	GCAACATTTGAAGCAGAGATCTGATTTAGAAAGAGCAAAAGCGCGTGAATGCTGTTT	1920
QY	2149	ACTTCTTCCAAATCAAAATCGGGTAAAGAGAGCAAAAGCGCGTGAATGCTGTTT	2208
DB	1921	ACTTCTTCCAAATCAAAATCGGGTAAAGAGAGCAAAAGCGCGTGAATGCTGTTT	1980
QY	2209	TCCAAATTTAGTGGATGTTTATCAGATGAATTTTCTCGATGAAAGCGAGATTTGTC	2268
DB	1981	TCCAAATTTAGTGGATGTTTATCAGATGAATTTTCTCGATGAAAGCGAGATTTGTC	2040
QY	2269	GAGAAATCAAAATCGGAGCGACTCAGTATGAGCGGAATTTACTTCAAGATCCAAAC	2328
DB	2041	GAGAAATCAAAATCGGAGCGACTCAGTATGAGCGGAATTTACTTCAAGATCCAAAC	2100
QY	2329	TTGAGAGGATCAATAGACACAGACCGTGGCTGGAGGAGAGTACAGATTTACCATC	2388
DB	2101	TTGAGAGGATCAATAGACACAGACCGTGGCTGGAGGAGAGTACAGATTTACCATC	2160
QY	2389	CAAGAGGATGACGATTTCAAGAGAGATTTACGTCACACTACCGGTACCGTTGATGAG	2448
DB	2161	CAAGAGGATGACGATTTCAAGAGAGATTTACGTCACACTACCGGTACCGTTGATGAG	2220
QY	2449	TCCTATCCAACTGTTTATTCAGAAATAGATGAGTGGAAATTTAAAGCTTATACCGT	2508
DB	2221	TCCTATCCAACTGTTTATTCAGAAATAGATGAGTGGAAATTTAAAGCTTATACCGT	2280
QY	2509	TATGATTAAGAGGATATTCAGAGATGATCAGACTTAGAAATCTATTTGATCGGTAC	2568
DB	2281	TATGATTAAGAGGATATTCAGAGATGATCAGACTTAGAAATCTATTTGATCGGTAC	2340
QY	2569	AATGCAAAACACAGAAATAGTAAATGTCGAGGACGAGTTCCTTATGCGCGTTTCAGCC	2628
DB	2341	AATGCAAAACACAGAAATAGTAAATGTCGAGGACGAGTTCCTTATGCGCGTTTCAGCC	2400
QY	2629	CAAGTCCAAATCGGAAAGTGTGAGAGCCGAAATCGATGCGGCGCACACTTGAATGAAT	2688
DB	2401	CAAGTCCAAATCGGAAAGTGTGAGAGCCGAAATCGATGCGGCGCACACTTGAATGAAT	2460
QY	2689	CCTGATCTAGATTTGTTCTTCGCGAG 2711	
DB	2461	CCTGATCTAGATTTGTTCTTCGCGAG 2483	

QY	2089	GCAACATTTGAAGCAGAGATCTGATTTAGAAAGAGCAAAAGCGCGTGAATGCTGTTT	2148
DB	1861	GCAACATTTGAAGCAGAGATCTGATTTAGAAAGAGCAAAAGCGCGTGAATGCTGTTT	1920
QY	2149	ACTTCTTCCAAATCAAAATCGGGTAAAGAGAGCAAAAGCGCGTGAATGCTGTTT	2208
DB	1921	ACTTCTTCCAAATCAAAATCGGGTAAAGAGAGCAAAAGCGCGTGAATGCTGTTT	1980
QY	2209	TCCAAATTTAGTGGATGTTTATCAGATGAATTTTCTCGATGAAAGCGAGATTTGTC	2268
DB	1981	TCCAAATTTAGTGGATGTTTATCAGATGAATTTTCTCGATGAAAGCGAGATTTGTC	2040
QY	2269	GAGAAATCAAAATCGGAGCGACTCAGTATGAGCGGAATTTACTTCAAGATCCAAAC	2328
DB	2041	GAGAAATCAAAATCGGAGCGACTCAGTATGAGCGGAATTTACTTCAAGATCCAAAC	2100
QY	2329	TTGAGAGGATCAATAGACACAGACCGTGGCTGGAGGAGAGTACAGATTTACCATC	2388
DB	2101	TTGAGAGGATCAATAGACACAGACCGTGGCTGGAGGAGAGTACAGATTTACCATC	2160
QY	2389	CAAGAGGATGACGATTTCAAGAGAGATTTACGTCACACTACCGGTACCGTTGATGAG	2448
DB	2161	CAAGAGGATGACGATTTCAAGAGAGATTTACGTCACACTACCGGTACCGTTGATGAG	2220
QY	2449	TCCTATCCAACTGTTTATTCAGAAATAGATGAGTGGAAATTTAAAGCTTATACCGT	2508
DB	2221	TCCTATCCAACTGTTTATTCAGAAATAGATGAGTGGAAATTTAAAGCTTATACCGT	2280
QY	2509	TATGATTAAGAGGATATTCAGAGATGATCAGACTTAGAAATCTATTTGATCGGTAC	2568
DB	2281	TATGATTAAGAGGATATTCAGAGATGATCAGACTTAGAAATCTATTTGATCGGTAC	2340
QY	2569	AATGCAAAACACAGAAATAGTAAATGTCGAGGACGAGTTCCTTATGCGCGTTTCAGCC	2628
DB	2341	AATGCAAAACACAGAAATAGTAAATGTCGAGGACGAGTTCCTTATGCGCGTTTCAGCC	2400
QY	2629	CAAGTCCAAATCGGAAAGTGTGAGAGCCGAAATCGATGCGGCGCACACTTGAATGAAT	2688
DB	2401	CAAGTCCAAATCGGAAAGTGTGAGAGCCGAAATCGATGCGGCGCACACTTGAATGAAT	2460
QY	2689	CCTGATCTAGATTTGTTCTTCGCGAG 2711	
DB	2461	CCTGATCTAGATTTGTTCTTCGCGAG 2483	

RESULT 12

US-09-997-914-29
; Sequence 29, Application US/09997914
; Publication No. US20030119159A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
; CURRENT APPLICATION NUMBER: US/09/997,914
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 29
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-997-914-29

Query Match 55.3%; Score 1498.2; DB 11; Length 3579;
Best Local Similarity 77.5%; Pred. No. 1.1e-310;

QY 1330 TTATCAATTCCTACTTTACGATTAATTAACAGCAACCTTGCAGCGCCACCACTTTTAATTTA 1389
DB 1081 ACATTAATCGTCCACTTTATATAGAGACCTTTTAAATATAGGGATAAATAATCAACAATA 1140
QY 1390 CGTGGTGGTCAAGAGTAGAATTTCT- - - - -ACACCTACAATAGCTTTACG- - - - - 1437
DB 1141 TCTGTTCTTACCGGACAGAAATTTGCTTATGGAACCTTCTCAAAATTTGCCATCCGCTGTA 1200
QY 1438 TATGCAAGGAAGAGGTACGGTGTGATTCCTTAACTGAATTAACCGCTCAGGATATATGTTG 1497
DB 1201 TACAGAAAAGCGGACGGTAGAATTCGCTGGATGAATATACCGCACAGATAACAAGTG 1260
QY 1498 CCACCTCGGAAGAGATATAGTCATCGTTTATGTCATGCAACTTTTGTTC- - - - -AA 1548
DB 1261 CCACCTAGGCAAGGATTTAGTCATCGAATTAAGCCATGTTTCAATGTTTCTGTCAGGCTTT 1320
QY 1549 AGATCTGGACACCTTTTAACTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1608
DB 1321 AGTAATAGTAGTGTAAAGTATAATAGAGCTCTTATGTTCTTCTTGGATACATCGTAGTGCA 1380
QY 1609 ACTCTTCAAAATACAATTCGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTT 1668
DB 1381 ACTCTTCAAAATACAATTCGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTT 1440
QY 1669 AGATTTGGGGGGGCACTCTGTGCTTATACAGGACCAAGGATTTTACAGGAGGGATATCCTT 1728
DB 1441 AGATTTGGGGGGGCACTCTGTGCTTATACAGGACCAAGGATTTTACAGGAGGGATATCCTT 1500
QY 1729 CGAAGAAATACCTTTGGTGTGATTTGTTATCTCTACAAGTCAATTAATTAATTAATTAAT 1788
DB 1501 CGAAGAAATACCTTTGGTGTGATTTGTTATCTCTACAAGTCAATTAATTAATTAATTAAT 1560
QY 1789 CAAAGATACCGTTTAAAGATTTCTGATCGTTCAGTAGGATGACAGGATTAATTAATTA 1848
DB 1561 CAAAGATACCGTTTAAAGATTTCTGATCGTTCAGTAGGATGACAGGATTAATTAATTA 1620
QY 1849 ACAGGAGCGGATCCACAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTTCAGAAA 1908
DB 1621 ACAGGAGCGGATCCACAGAGTGGGAGGCCAAGTTAGTGTAAATTAATTAATTAATTAAT 1680
QY 1909 ACTATGGAATAGGGAGAGACTTAACATCTAGAACATTTAGATATACCGATTTAGTAAT 1968
DB 1681 ACTATGGAATAGGGAGAGACTTAACATCTAGAACATTTAGATATACCGATTTAGTAAT 1740
QY 1969 CTTTTTTCATTTAGAGCTAATCCAGATATAATTTGGGATAGTGAACACTCTATTGCT 2028
DB 1741 CTTTTTTCATTTAGAGCTAATCCAGATATAATTTGGGATAGTGAACACTCTATTGCT 1800
QY 2029 GCAGGTTCTATTAGTAGCGTTGAACCTTTATATAGATAAAATTTGAATTTCTTAGCAGAT 2088
DB 1801 GCAGGTTCTATTAGTAGCGTTGAACCTTTATATAGATAAAATTTGAATTTCTTAGCAGAT 1860
QY 2089 GCACATTTTGAAGCAATCTGATTTTGAAGAGCAACAAAGCGGTGAATGCCCTGTTT 2148
DB 1861 GCAACATTTTGAAGCAATCTGATTTTGAAGAGCAACAAAGCGGTGAATGCCCTGTTT 1920
QY 2149 ACTCTTCCAATCAATCGGTTTAAACCGATGTGACGATTTATCATATTTGATCAAGTA 2208
DB 1921 ACTCTTCCAATCAATCGGTTTAAACCGATGTGACGATTTATCATATTTGATCAAGTA 1980
QY 2209 TCCAAATTTAGTGGATTTTATCAGATGAATTTTGTGCGATGAAGAGGAGAAATTTGCC 2268
DB 1981 TCCAAATTTAGTGGATTTTATCAGATGAATTTTGTGCGATGAAGAGGAGAAATTTGCC 2040
QY 2269 GAGAAAGTCAAAATCGGAGCGGACTCAGTGTATGAGCGGAAATTTACTTCAAGATCCAAAC 2328
DB 2041 GAGAAAGTCAAAATCGGAGCGGACTCAGTGTATGAGCGGAAATTTACTTCAAGATCCAAAC 2100
QY 2329 TTCAGAGGATCAATAGACAAACGACCGTGGCTGGAGAGGAGTACAGATATTACCATC 2388
DB 2101 TTCAGAGGATCAATAGACAAACGACCGTGGCTGGAGAGGAGTACAGATATTACCATC 2160

QY 2389 CAAGGAGGAGATGACGTATTTCAAAGAGAAATTACGTCACTACCGGTTACCGTTGATGAG 2448
DB 2161 CAAGGAGGAGATGACGTATTTCAAAGAGAAATTACGTCACTACCGGTTACCGTTGATGAG 2220
QY 2449 TCGTATCCAACGTATTTATATCAGAAATAGATGAGTCAAAATTAAGCTTATACCCGT 2508
DB 2221 TCGTATCCAACGTATTTATATCAGAAATAGATGAGTCAAAATTAAGCTTATACCCGT 2280
QY 2509 TATGAATTAAGAGGGTATATCAGAAATAGTCAAGACTTAAAGATCTATTGATCGGTAC 2568
DB 2281 TATGAATTAAGAGGGTATATCAGAAATAGTCAAGACTTAAAGATCTATTGATCGGTAC 2340
QY 2569 AATGCAAAACACGAAATAGTAAATGTGCCAGCACGGTTCCTTATGCGCGTTTCAGCC 2628
DB 2341 AATGCAAAACACGAAATAGTAAATGTGCCAGCACGGTTCCTTATGCGCGTTTCAGCC 2400
QY 2629 CAAAGTCCAATCGGAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT 2688
DB 2401 CAAAGTCCAATCGGAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGAATGGAAT 2460
QY 2689 CCTGATCTAGATTTGTTCTTCGAG 2711
DB 2461 CCTGATCTAGATTTGTTCTTCGAG 2483

RESULT 13

US-10-365-645-29
; Sequence 29, Application US/10365645
; Publication No. US20030182682A1
; GENERAL INFORMATION:
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Malvar, Thomas
; TITLE OF INVENTION: Antibodies Immunologically Reactive with Broad-Spectrum
; TITLE OF INVENTION: Delta-Endotoxins (Amended)
; FILE REFERENCE: 11792.0210.DVUS02 (MECO:210--3)
; CURRENT APPLICATION NUMBER: US/10/365,645
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 09/873,873
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-10-365-645-29

Query Match 55.3%; Score 1498.2; DB 12; Length 3579;
Best Local Similarity 77.5%; Pred No. 1.1e-310;
Matches 1924; Conservative 0; Mismatches 508; Indels 51; Gaps 7;

QY 259 AATCAATGCATACCTTACAATTTGTTTAAAGTAACTCTGAAGAGTAGTACTTTTGGATGGAGAA 318
DB 22 AATGAATGCATTCCTTATAATTTGTTTAAAGTAACTCTGAAGTAGAAGTATTAGTGGAGAA 81
QY 319 CGGATATCAACCTGGTAATTAATCTCTGTCTACTTGTCTCAGTTCTGTTTCTGGTA 378
DB 82 AGAATAGAACTGGTTACACCCCAATCGATATTTCTTGTCTGCTAACCGAATTTCTTTTG 141
QY 379 TCTAACTTTGTACACGAGGGAGGATTTTGTAGTTGATTAATAGATTTCGTATGGGGAATA 438
DB 142 AGTGAATTTGTTCCGGTGTGGATTTGTGTAGGACTAGTTGATATAATATATGGGAAT 201
QY 439 GTTGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTAATTAATTAATTAATGAAGA 498

Wed Oct 15 11:56:12 2003

Db 202 TTGTGTCCTCTCAATGGACGCAATTTCTGTACAAATTAAGACAGTTAAATTAACCAAGA 261
 Qy 499 ATAGCTGAATTTGCTAGGAATCTGCTATTTGCTAATTAATTAAGAGGATTAAGAAACAATTC 558
 Db 262 ATAGAGAAATTCGCTAGGACCAAGCAATTTCTAGATTAAGAGGACTAAGCAATCTTTAT 321
 Qy 559 ANTATATATGTGGAGCAATTTAAAGAAATGGGAAGAGATCCTTAATAATCCAGCAACGAG 618
 Db 322 CAATTTAGCAGATCTTTTACAGAGTGGGAAGCAGATCCTACTAATCCAGCAATTAAGA 381
 Qy 619 ACCAGATTAATGTATCGCTTCGTATCTATCTGATGGCTACTTGAAGAGGACATTTCTTCG 678
 Db 382 GAAGAGATGGTATTCATTCATGACATGACAGTGCCTTACACCGCTATTTCTCTT 441
 Qy 679 TTTCGAATTTCTGGATTTGAGTACCCCTTTTATCCGTTTATCTCCTCAAGCGGCAATCTG 738
 Db 442 TTTCGAGTTCAAAATTTATCAAGTTCTCTTTATCAGTATATGTTCCAGCTTCAAGCTGCAAAATTA 501
 Qy 739 CATCTAGCTATATTAAGAGATCTGTAAATTTTGGAGAAAGATTTGGATTTGACACGATA 798
 Db 502 CAATTTACGTTTGGAGATGTTTCAGTGTGGACAAAGGTGGGATTTGATGCCGOG 561
 Qy 799 AATGTCAATGAAGCAATATAATAGACTAATTTAGGCAATTTGATGATATCTGATCAGTGT 858
 Db 562 ACTATCAATAGTCTGTATAATGATTTAACTAGCTTTATGGCACTATACAGATTAATGCT 621
 Qy 859 GCAATACGTATATTCGGGATTAATAATTTACCGAATCTAGCTATCAAGATTTGGATA 918
 Db 622 GTACGCTGTACAAATACGGGATTTAGAACGTGTATGGGACCGGATTTAGAGATTTGGTA 691
 Qy 919 ACATATATCGATTTACGGAGAGACTTAACATGACTGATTTAGATATTCGCGCTTTCTT 978
 Db 682 AGGTATATCAATTTAGAAAGAAATTAACACTAATCTGATTTAGATATCTGCTCTGTC 741
 Qy 979 CCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGTCAACTAACAGAGGAGTT 1038
 Db 742 CCGAATATGATAGTAGAAGATATCCAAATTCGAACAGTTTCCAAATTAACAGAGAAAT 801
 Qy 1039 TATAGGACCAATTAATTAATTTAATCCAGTTACAGTCTGTAGCTCAATTAACCTACT 1098
 Db 802 TATACAAACCCAGTATTAAGA-----AAATTTGATGATGTTTTCAGGC 846
 Qy 1099 TTTAACGTTATGGAGAGAGCGCAATTAAGAAATCTCATTTATTTGATATTAATTAAT 1158
 Db 847 TCGGCTCAGGCAATAGAAAGAGATTTAGGAGTCCACATTTGATGATATTAACAGT 906
 Qy 1159 CTTACAACTTTACGATTTGTTAGTGTGGACGCAATTTTATTTGGGGAGCAATCGA 1218
 Db 907 ATAAACATCTATACGATGCTCATAGG-----GTTATTAATTTGTTGTCAGGCGCATCA 960
 Qy 1219 GTAAATCTAGCCTTATAG-----AGTGGTAAACATAACATCTCTATATATGGAAGA 1272
 Db 961 ATATAGGCTTCTCTGTAGGTTTCGGGGCCAGAAATTCATTTCCGCTATATGGAAT 1020
 Qy 1273 GAGGCAACGAGGAGCTTCAAGATCTTTACTTTTAA---TGGACCGTATTTAGGACT 1329
 Db 1021 ATGGGAAATGCAAGCTTCACAAACAAAGTATTTGCTCAACTAGTTCAGGCGGTATAGA 1080
 Qy 1330 TTATCAATTTCTACTTTACGATTTATAGCAACCTTCCAGCGCCACATTTTAAATTA 1389
 Db 1081 ACATATGCTTCCACTTTATATAGAGACCTTTTAAATAGGATTAATAATTAACAACTA 1140
 Qy 1390 CGTGTGGTGAAGAGATTAAGTTTCT-----ACACCTACAAATAGCTTTAG----- 1437
 Db 1141 TCTGTCTTCTGAGGAGACAGAAATTTGCTATGGAACCTCTCAATTTGCCATCCGCTGTA 1200
 Qy 1438 TATCGAGGAGAGGATTCGTTGATTTCTTTACTGAATTTACGCTCAGGATTAATAGTGTG 1497
 Db 1201 TACAGAAAGAGGAGACGCTAGATTTGCTGGATGAATATACGCAAGATTAACAGCTG 1260
 Qy 1498 CCACCTCGGAAGGATATAGTCATCGTTTATGTCAGTCTTTGCTC-----AA 1548
 Db 1261 CCACCTAGGACGAGATTTAGTCATGATTAAGCCAGTTTCAATGTTTCTTCAGGCTTT 1320

Qy 1549 AGATCTGGAACACCTTTTAAACAACTGGGTAGTATTTTCTTGAGCGCAATCTGTAGTGA 1608
 Db 1321 AGTAATAGTAGTGAAGTATAATTAAGAGCTCTCTATGTTCTCTTGATATACATCGTAGTGA 1380
 Qy 1609 ACTCTTCAAAATCAATTAATTCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGTTT 1668
 Db 1381 ACTCTTCAAAATCAATTAATTCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGTTT 1440
 Qy 1669 AGAGTTTGGGGGGGACCTCTGTCTATTAAGAGAGAGGATTTTACAGAGAGGATATTCCTT 1728
 Db 1441 AGAGTTTGGGGGGGACCTCTGTCTATTAAGAGAGAGGATTTTACAGAGAGGATATTCCTT 1500
 Qy 1729 CGAGAAATACCTTTGGTCTGATTTTGTATCTCTCAAAAGTCAATTAATTAATCAAAATAC 1788
 Db 1501 CGAGAAATACCTTTGGTCTGATTTTGTATCTCTCAAAAGTCAATTAATTAATCAAAATAC 1560
 Qy 1789 CAAAGATACCGTTTGAAGTTCGTAGCTTCCAGTAGGATTCAGAGAGTATTAAGTATTA 1848
 Db 1561 CAAAGATACCGTTTGAAGTTCGTAGCTTCCAGTAGGATTCAGAGAGTATTAAGTATTA 1620
 Qy 1849 ACAGAGCGGATCCACAGAGTGGGAGGCGGAGTGTAGATATGCTCTCTTCAGAAA 1908
 Db 1621 ACAGAGCGGATCCACAGAGTGGGAGGCGGAGTGTAGATATGCTCTCTTCAGAAA 1680
 Qy 1909 ACTATGGAATAAGGGGAGAACTTAACATCTAGACATTTAGATATACCGATTTAGTAA 1968
 Db 1681 ACTATGGAATAAGGGGAGAACTTAACATCTAGACATTTAGATATACCGATTTAGTAA 1740
 Qy 1969 CTTTTTCAATTTAGAGCTTAATCCAGATTAATTCGGATTAAGTGAACACCTCTATTTGTT 2028
 Db 1741 CTTTTTCAATTTAGAGCTTAATCCAGATTAATTCGGATTAAGTGAACACCTCTATTTGTT 1800
 Qy 2029 GCAGGTTCTATTTAGTGTAGCTTTGAATTTATATAGATAAAATTTGAATTTATTTAGCAGAT 2088
 Db 1801 GCAGGTTCTATTTAGTGTAGCTTTGAATTTATATAGATAAAATTTGAATTTATTTAGCAGAT 1860
 Qy 2089 GCACATTTTGAAGCAGAACTCTGATTTTGAAGAGACACAAAGGCGGTGAATGCTCTGTT 2148
 Db 1861 GCACATTTTGAAGCAGAACTCTGATTTTGAAGAGACACAAAGGCGGTGAATGCTCTGTT 1920
 Qy 2149 ACTCTTCAATCAAAATCGGTTAAAAACCGATGTGACGATTTATCATATGATCAAGTA 2208
 Db 1921 ACTCTTCAATCAAAATCGGTTAAAAACCGATGTGACGATTTATCATATGATCAAGTA 1980
 Qy 2209 TCCAAATTTAGTGTGATTTTATCAGATGAATTTTCTGATGAAAGAGAGAAATTTGTC 2268
 Db 1981 TCCAAATTTAGTGTGATTTTATCAGATGAATTTTCTGATGAAAGAGAGAAATTTGTC 2040
 Qy 2269 GAGAAAGTCAACATGCGAAGCGACTCAGTGTAGAGCGAAATTTACTTCAAGATCCAAAC 2328
 Db 2041 GAGAAAGTCAACATGCGAAGCGACTCAGTGTAGAGCGAAATTTACTTCAAGATCCAAAC 2100
 Qy 2329 TTCAGAGGATCAATAGACACAGACCGGTGGCTGGAGAGAGTACAGATATTAACATC 2388
 Db 2101 TTCAGAGGATCAATAGACACAGACCGGTGGCTGGAGAGAGTACAGATATTAACATC 2160
 Qy 2389 CAAAGAGAGATGAGCTTATTCAGAGAAATTTAGCTCAGACTACCGGTACCGTTGATGAG 2448
 Db 2161 CAAAGAGAGATGAGCTTATTCAGAGAAATTTAGCTCAGACTACCGGTACCGTTGATGAG 2220
 Qy 2449 TGTCTATCAACGTTATTTATTCAGAGAAATTTAGCTCAGAAATTAAGAGCTTATACCGGT 2508
 Db 2221 TGTCTATCAACGTTATTTATTCAGAGAAATTTAGCTCAGAAATTAAGAGCTTATACCGGT 2280
 Qy 2509 TATGAATTAAGAGGATATTCAGAGAGTACAGACTTAGAATCTATTTGATCGGCTAC 2568
 Db 2281 TATGAATTAAGAGGATATTCAGAGAGTACAGACTTAGAATCTATTTGATCGGCTAC 2340
 Qy 2569 AATGCAGAAACGAAATAGTAAATGTCGAGGACCGGTTCTTATGCGCGCTTTCAAGCC 2628
 Db 2341 AATGCAGAAACGAAATAGTAAATGTCGAGGACCGGTTCTTATGCGCGCTTTCAAGCC 2400

=Db

Qy	2629	CAAGTCCAAATCGAARAGTGTGGNGRACCGAATCGATCGCGCCACACCTTGAAATGGAAT	2688
Db	2401	CAAAAGTCCAAATCGAARAGTGTGGNGRACCGAATCGATCGCGCCACACCTTGAAATGGAAT	2460
Qy	2689	CCTGATCTAGATTGTTCTCTCGAG	2711
Db	2461	CCTGATCTAGATTGTTCTCTCGAG	2483

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RESULT 14
US-09-826-660-19
; Sequence 19, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-19

```

Query Match 50.4%; Score 1366.2; DB 9; Length 1860;
Best Local Similarity 83.4%; Pred. No. 1.6e-282;
Matches 1551; Conservative 0; Mismatches 308; Indels 0; Gaps 0;

241	QY	ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATTTGTTTAAGTAAATCTCGAAGAA	300
1	DB	ATGGAGGAGAAACAATCAGAAATCAGTGCATACCTTACAACTGCTTGAGCAATCTCTGAAGAG	60
301	QY	GTACTTTTCGGATGGGAAACGGGATACCAACTGTAATTACTCAATTGCATATTTCTCTGTCA	360
61	DB	GTACTTCTTGATGGGAAACGGATCTCAACTGGTAACCTTAGCAATTGACATCTCACTGTCA	120
361	QY	CTTGTTTCAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTTAGTTGGATTAATA	420
121	DB	CTTGTTTCAGTTTCTTGCTCTCAACTTTGTTCCAGGGGGTGGCTTTCTTGTTGGACTCAT	180
421	QY	GAATTTGATGGGGAATAGTTGGCCCTCTCAATGGGATGCATTTCTAGTACAAATTTGA	480
181	DB	GACTTTGTGTGGGGCAATTTGTGGCCCATCTCAATGGGATGCCTTTCTTGACAGATTGAA	240
481	QY	CAATTAATTAATGAAAGAAATAGCTGAATTTGCTTAGGAATGCTGCTATTTGCTAATTTAGAA	540
241	DB	CAGTTTGATCAATGAGAGGATAGCTGAGTTTGCTAGGAATGCTGCCAATTTGCCAATCTGGAA	300
541	QY	GGATTAGGAAACAATTTCAATATATATGTGGAGCATTTAAAGATGGGAGNAGNATCT	600
301	DB	GGATTGGGAAACAATTTCAACATCTATGTGGAAGCCTTCAAGAAATGGGAGAGAGATCC	360
601	QY	AATAATCCAGCAACGAGGACGAGATTAATTCGCTTTTCGTATCTTGATGGGCTACTT	660
361	DB	AACAATCCAGCAACCCGTAACGAGAGTCAATTCGCTTTTCGGATACTTGATGGGCTACTT	420
661	QY	GAAAGGCAATTCCTTCGTTTCGAAATTTCTGGATTGGAATGTAACCCCTTTTATCCGGTTTAT	720
421	DB	GAAAGGCAATTCCTTCGTTTCGAAATTTCTGGATTGGAATGTAACCCCTTTTATCCGGTTTAT	480

Qy	721	GCTCAAGCGGCGCAATCTGCATCTAGCTATATTAAGAGANTTCTGTAAATTTTTTGGAGAAAGA	780
Db	481		
		GCTCAAGCTGCGCAATCTGCATCTTGGCAATCTAAGAGATTCTGTGATCTTTGGAGAAAGA	540
Qy	781	TTGGGATTTGACNACGATAAATGTCTCAATGAAAACCTATATATAGACTTAATTAGGCATATTGAT	840
Db	541		
		TGGGGATTGACAACATATCAATATGTCAATGAGAACTTACAACAGACTCTCATCAGACACATTTGAT	600
Qy	841	GAATATGCTGATCACTGTGCAAAATACGTATAATCGGGGATTTAAATTAATTTTACCAGAAATCT	900
Db	601		
		GAGTATGCTGATCACTGTGCGCAACCTACAAATCTGTGCTCTCAACAACTTTACCGAAGTCT	660
Qy	901	ACGTATCAAGATTGGATAACATATAATTCGATTACGGAGAGACTTAAACATTTGACTGTATTA	960
Db	661		
		ACGTATCAAGATTGGATCACCTCAATTCGATTTCAGGAGGATCTCTCAATTTGACTGTCTTG	720
Qy	961	GATATCGCGCTTCTTTTCCAACTATGACAAATAGGAGATATCCAATTCAGCCAGTTGGT	1020
Db	721		
		GACATTCCTGCTTTCTTTCCAACTATGACAAACAGAGATATCCCAATTCACACAGTTGGT	780
Qy	1021	CAACTAAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAACTCACAGTTTACAGTCT	1080
Db	781		
		CAACTAAACAGGGAAGTTACATGATCCACTCATCAATTCATCCAGTTTACAACT	840
Qy	1081	GTAGTCAATTAACCTACTTTTAAAGTTATGGAGAGACGCGCAATTAGAAATTCCTCAATTA	1140
Db	841		
		GTTGCTCAGTTACCTACTTTCAATGTGATGGAAGCTCAGCCATCAGGAATCCACACTTG	900
Qy	1141	TTTTGATATTTGAATTAATCTTACAACTTTTACGGATTGGTTTAGTTTGTGGACCGCAATTTT	1200
Db	901		
		TTTGACATTTCTCAACAACTTTTACCATCTTCACCTGATTTGGTTTCAAGTGTGGACCGCACTTC	960
Qy	1201	TATTTGGGGAGACATCGAGTAATATCTAGCCTTTATAGGAGTGGTAACATAACATCTCCT	1260
Db	961		
		TACTGGGGTGAACATCGTGTGATCTCTAGCTTGATAGTGGAGGTAAACATCATCTCCT	1020
Qy	1261	ATATATGGAAGAGAGCGGCAACGAGGACCTCCAAAGTCTCTTTACTTTTAAATGACCGGTA	1320
Db	1021		
		ATCTATGTTAGGGAGCGCAATCAGGAGCCTCCAAGATCTCTTCACTTTCAATGACCGGTC	1080
Qy	1321	TTTTAGGACTTTATCAATTCCTACTTTTACGATTATACGCAACCTTCCGCGCCACCAT	1380
Db	1081		
		TTCAGGACTTTGTCCAACTCCTCTTTGCGATTGTTTAAACAACCATTTGGCGTGTCTCACCA	1140
Qy	1381	TTTAAATTAAGTGGTGTGAAGGATAGAAATTTCTACACCTTCAAAATAGCTTTACGTAT	1440
Db	1141		
		TTCAACTTACGTGGTGTGAAGGATAGATTTCTCAACACCCACCAACGTTTCAAGTAT	1200
Qy	1441	GCAGGAAGAGGTACGGTTGATCTTTTAACTGAATTAACCGCTGAGGATAAATAGTGTGCCA	1500
Db	1201		
		CGTGGAAAGAGGTCAAAGTTGATTCGTTGACTGAGTTACCGCTGAGGACAACTCAGTTCCA	1260
Qy	1501	CCTTCGGAAGGATATAGTCATCGTTTATGTCTACGCACTTTTGTTCAAAGATCTGGAACA	1560
Db	1261		
		CCTTCGGAAGGCTACAGTCATCGTCTGTCTGTCGCAACCTTTGTTCAAAAGGTCGGAACA	1320
Qy	1561	CCTTTTAAACAACCTGCTGTAGTATTTTCTTGAACGCATCGTAGTGCACCTCTTACAAAT	1620
Db	1321		
		CCGTTCTTGACAACTGGTGTGTCTCTCTGCGACTCTGAGCGCACTCTTACCAAC	1380
Qy	1621	ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG	1680
Db	1381		
		ACCAATTTGATCCAGAGAGGATCAATCAGATACCTCTTTGTGAAGGCTTCAGAGTTTGGGG	1440
Qy	1681	GGCACCTCTGTCAATTACAGGACAGATTTTACAGGAGGGGATATCCTTCGAGAAATACC	1740
Db	1441		
		GGCACCTCTGTGATCACCCGTCAGGATTCACAGGAGGGGACATCTTTCGACGCAACACC	1500
Qy	1741	TTTTGGTGAATTTGTATCTCTTACAAGTCAATATTAATTTTCAACCAATTAACCAAGATACCCT	1800
Db	1501		
		TTTTGGTGACTTTGTATCTCTTCAAGTCAACATCACTCACCCATCAACAAAGATACCCT	1560
Qy	1801	TTAAGATTTTCGTTACGCTTCCATAGGGATGACGAGTTTATAGTATTTTACGAGCGGCA	1860

Db 1256 TAGAAGACCTTTTAATATAGGGATAAATATCAACAACATATCTGTTCTTGACCGGACAGA 1315
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Db 1316 ATTTGCTTATGGAACCTCTCTCAATTTGCCATCGCTGTATACAGAAAAAGCGAACGGT 1375
Qy 1458 TGATTTCTTTAACTGAATACCGCTGAGGATATAGTGTGCACTCGCGAAGGATATAG 1517
Db 1376 AGATTGCGTGGATGAATACCGCACAGATAACAACGTGCCACCTTAGGCAAGGATTTAG 1435
Qy 1518 TCATCGTTTATGTCAATGCACTTTTGTTCAA-----AGATCTGGAACACCTTTTTT 1568
Db 1436 TCATCGATTAAAGCATGTTTCAATGTTTCTGTCAGGCTTTAGTAATAGTGTAGTAT 1495
Qy 1569 AACAACTGGTGTAGTATTTCTTTGGACGATCGTAGTCAACTTTTACAATAACAATTGA 1628
Db 1496 AATAAGAGCTCTCTATGTTCTCTTGGATACATCGTAGTGTGAATTTAATAATATAATCC 1555
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Qy 1809 TCGTTACGCTTCAGTAGGGATGACAGGATTTAGTATTTAAACAGGAGCGCATCCACAGG 1868
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Qy 1869 AGTGGAGCCCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGCAAAATAGGGAGAA 1928
Db 1775 AATTGACGAAGACCTTATTAATCAGGGAAATTTTCAGCACTATGAGTAGTGGGAGTAA 1834
Qy 1929 CTTAACATCTAGAACATTTAGATATACCGAATTTAGTAATCTTTTTCATTTTAGAGCTAA 1988
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Qy 1989 TCCAGATATAATTGGGATTAAGTGAACAACCTCTATTTGGTGCAGGTTCTATTAGTAGCT 2048
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Qy 2049 TGAACCTTTATATAGATAAAATTTGAATTTATCTAGCAGATGCAACATTTGAAGCAGATC 2108
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Qy 2109 TGATTTAGAAAGACACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAATCAAAATCGG 2168
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Qy 2469 TCAGAAAAATAGATGAGTCGAAATTTAAAGCTTTATATCCCGTTATGAAATTAAGAGGTATAT 2528
Db 2360 TCAGAAAAATAGATGAGTCGAAATTTAAAGCTTTATATCCCGTTATGAAATTAAGAGGTATAT 2419
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Qy 2649 TG 2650
Db 2540 TG 2541

Search completed: October 13, 2003, 13:53:14
Job time : 2266 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on: October 9, 2003, 13:26:09 ; Search time 76 Seconds
(without alignments)
1744.851 Million cell updates/sec

Title: US-09-918-485-2

Perfect score: 4358

Sequence: 1 MEENNQICIPYNCLSNPBE.....GPNRCAPLEWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 60053 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4358	100.0	823	11	US-09-918-485-2
2	4289	98.4	1189	11	US-09-972-175-12
3	4288	98.4	1189	11	US-09-972-175-2
4	4288	98.4	1189	11	US-09-972-175-6
5	4287	98.4	1189	11	US-09-972-175-4
6	4283	98.3	1189	11	US-09-972-175-10
7	4282	98.3	1189	11	US-09-972-175-8
8	4282	98.3	1189	11	US-09-972-175-59
9	4281	98.2	1189	11	US-09-972-175-61
10	4111.5	94.3	1163	9	US-09-826-660-21
11	3088	70.9	1193	9	US-09-973-873-30
12	3088	70.9	1193	11	US-09-997-914-30
13	3088	70.9	1193	12	US-10-365-645-30
14	2537	58.2	1177	9	US-09-873-873-10
15	2537	58.2	1177	9	US-09-873-873-12

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18	2537	58.2	1177	11	US-09-997-914-12
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23	2535	58.2	1177	9	US-09-873-873-26
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34	2492	57.2	1177	12	US-10-365-645-28
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36	2491	57.2	1181	11	US-09-988-462-15
37	2438	55.9	1177	9	US-09-873-873-34
38	2438	55.9	1177	12	US-10-365-645-34
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41	2367.5	53.8	1179	15	US-10-035-060-4
42	2346	53.6	1178	9	US-09-851-194-2
43	2334.5	52.0	1148	9	US-09-826-660-2
44	2266	52.0	1156	9	US-09-826-660-15
45	2264	52.0	1156	9	US-09-826-660-15

ALIGNMENTS

RESULT 1

US-09-918-485-2
; Sequence 2, Application US/09918485
; Publication No. US20030115628A1
; GENERAL INFORMATION:

APPLICANT: SANCHIS, Vincent
LERECLUS, Didier
MENO, Ghislaine
LECADET, Marguerite-Marie
MARTOURET, Daniel
DEPONDER, Raymond

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR

POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS

LEPIDOPTERA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,485

FILING DATE: 25-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/461,551

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US 08/251,652

FILING DATE: 31-MAY-1994

APPLICATION NUMBER: US 07/458,754

FILING DATE: 11-DEC-1989

Sequence 14, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 28, Appl
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Sequence 28, Appl
Sequence 6, Appl
Sequence 15, Appl
Sequence 34, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 6, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 15, Appl

APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-918-485-2

Query Match 100.0%; Score 4358; DB 11; Length 823;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEENNQCIPYCLNPEVLLDGERISTGSSIDISLVQFLVSNFVPGGFLVGLI 60
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Db 61 DFVWGVGSPQWDAFLVQIEQLINERIAEFARNAATANLEGNNFNIVYAEKWEEDP 120
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Db 121 NNPATRTVIDRFRILDGLLDRIDPSRISGFEVPLLSVYQAANLHAIIRDVSIFGER 180
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Db 181 WGLTTINVENNRLIRHIDEYADHCANTYNGLNLPKSTYQDMITYNRLRDLTLTVL 240
Qy 241 DIAAFPNYDNRYPQVQQLTREVTYDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFPNYDNRYPQVQQLTREVTYDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDLANNLTFTDWSVGRNFGYWGCHRVISLIGGNITSPYIGREANQEPFRFTNGVP 360
Db 301 FDLANNLTFTDWSVGRNFGYWGCHRVISLIGGNITSPYIGREANQEPFRFTNGVP 360
Qy 361 FRTLSTPTLRLLOQPCORHFNLRGEGVEFTPTNSFTYRGRGTVDLSLTELPPEDNSVP 420
Db 361 FRTLSTPTLRLLOQPCORHFNLRGEGVEFTPTNSFTYRGRGTVDLSLTELPPEDNSVP 420
Qy 421 PRGYSHRLCHATFVQSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PRGYSHRLCHATFVQSGTFLTTGVVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
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Db 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVINSPIQRYELFRYASSRDARVILTGAA 540
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Db 661 DCLSDFECLDEKRELSEKVKHAKELSDERNLLQDPNFGINRQPDGRWGRTDITIGGD 720

Qy 721 DVFKENYVTLFGTYDECTYLYQKIDSKKAYTRYELRGVIERSDQLEIYLIATNAKH 780
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Db 781 EIVNVPGTSLWPLSAQSPIGKGPENRCAPHLEWNPDLDCSC 823

RESULT 2
US-09-972-175-12
Sequence 12, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Glimmer, Amy Jelen
Mectus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-972-175-12

Query Match 98.4%; Score 4289; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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Db 1 MEENNQCIPYCLNPEVLLDGERISTGSSIDISLVQFLVSNFVPGGFLVGLI 60
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Db 61 DFVWGVGSPQWDAFLVQIEQLINERIAEFARNAATANLEGNNFNIVYAEKWEEDP 120
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RESULT 3
US-09-972-175-2
; Sequence 2, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-972-175-2

Query Match 98.4%; Score 4288; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1 MEENNQOCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFAFARNAAIANLEGIGNNFNIYVEAFKEWEDP 120
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Db 241 DIAAPPYNNRRYPIQPVQQLTRVYTDPLINFPQLQSVQALPTFNVMSSAIRNPHL 300
Qy 301 FDLNNLTITFDWFSVGRNFWGHRVSSLIIGGNITSPYIGREANQPPRSTFNGPV 360
Db 301 FDLNNLTITFDWFSVGRNFWGHRVSSLIIGGNITSPYIGREANQPPRSTFNGPV 360
Qy 361 FRTLSTPLRLLOQPCORHFNLRGEGVEFSTPNSFTYGRGTVDLSITELPPEDNSVP 420
Db 361 FRTLSTPLRLLOQPCORHFNLRGEGVEFSTPNSFTYGRGTVDLSITELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPPLTTGGVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQSRGTPPLTTGGVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
Qy 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAA 540
Db 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARVILVTGAA 540
Qy 541 STGVGGQVSNMPLQKTMELTSGRTYTDPSNPFSTRANPDIIIGISEQPLFCAGSI 600
Db 541 STGVGGQVSNMPLQKTMELTSGRTYTDPSNPFSTRANPDIIIGISEQPLFCAGSI 600
Qy 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSTDITIQGSD 720
Db 661 DCLSDFCCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSTDITIQGSD 720
Qy 721 DVFKENYVTLPGTVDECPYLYQKIDESKUKATRYELRGYIEDSQDLIELYLIYNAKH 780
Db 721 DVFKENYVTLPGTVDECPYLYQKIDESKUKATRYELRGYIEDSQDLIELYLIYNAKH 780
Qy 781 EIVNVPGTGLWPLSAQSPIGKGEPNRCAPHLEWNPDLDCSC 823

us-09-918-485-2.rapb

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781 EIVNPGTSLWPLSAQSPGKCBPNCAPHLWPNPDLDCSC 823

Db

RESULT 4

US-09-972-175-6
; Sequence 6, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-972-175-6
Query Match 98.4%; Score 4288; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENQOCIPYNCLSNPPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENQOCIPYNCLSNPPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIVGSPQDAFLVQICOLINERIAEFARNAIAINLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFVWGIVGSPQDAFLVQICOLINERIAEFARNAIAINLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPTATRVTRIDRFLDGLERDIPSRISGFEVPLSVQAQANLHLAIRDSDVIFGER 180
Db 121 NNPTATRVTRIDRFLDGLERDIPSRISGFEVPLSVQAQANLHLAIRDSDVIFGER 180
QY 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNGLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNGLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFPNYNNRYPPIQPVGQLTRVYTDLINFPOLQSVQAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFPNYNNRYPPIQPVGQLTRVYTDLINFPOLQSVQAQLPTFNWESSAIRNPHL 300

QY 301 FDIANNLTFTDFSVGCRNFYWGHRVVISSLLGGNTTSITVCRANOEPPRSFTENGVP 360
Db 301 FDIANNLTFTDFSVGCRNFYWGHRVVISSLLGGNTTSITVCRANOEPPRSFTENGVP 360
QY 361 FRTLSIPTLRLLQQPCQRHHFNLRGGVEFTPTNSFTYRGRTVDSLTELPEPDSVP 420
Db 361 FRTLSIPTLRLLQQPCQRHHFNLRGGVEFTPTNSFTYRGRTVDSLTELPEPDSVP 420
QY 421 PREGYSHRLCHATFVQSGTPTLTGTVFSWTHRSATLNTIDPERINOIPLVKGFRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPTLTGTVFSWTHRSATLNTIDPERINOIPLVKGFRVWG 480
QY 481 GTSVITGPGFTGDIILRRNTGDFVSLQVNINSPIQYRLRFYASSRDARVILTGAA 540
Db 481 GTSVITGPGFTGDIILRRNTGDFVSLQVNINSPIQYRLRFYASSRDARVILTGAA 540
QY 541 STVGGOVSVNMPLOKTMWIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQLFAGSI 600
Db 541 STVGGOVSVNMPLOKTMWIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQLFAGSI 600
QY 601 SSGELYIDKIEILLADATPEAESDLERAQAVNALFTSSNQIGLKTDTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEILLADATPEAESDLERAQAVNALFTSSNQIGLKTDTVDYHIDQVSNLV 660
QY 661 DCLSDPCLDEKRELSKVKHAKRLSDERNLLODPNFRGINRQPDGRWGSGTDITIQGD 720
Db 661 DCLSDPCLDEKRELSKVKHAKRLSDERNLLODPNFRGINRQPDGRWGSGTDITIQGD 720
QY 721 DVFKNYVTLGTVDECYTYLYOKIDESKLVKATRYELRGVIEDSQLEIYLIYNAKH 780
Db 721 DVFKNYVTLGTVDECYTYLYOKIDESKLVKATRYELRGVIEDSQLEIYLIYNAKH 780
QY 781 EIVNPGTSLWPLSAQSPGKCBPNCAPHLWPNPDLDCSC 823
Db 781 EIVNPGTSLWPLSAQSPGKCBPNCAPHLWPNPDLDCSC 823

RESULT 5

US-09-972-175-4
; Sequence 4, Application US/09972175
; Publication No. US20030101482A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,175
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/337,635
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MECO:206
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-972-175-4

Query Match 98.4%; Score 4287; DB 11; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 MEENNQCIPYCNLSNPEVLLDGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYCNLSNPEVLLDGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60

QY 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAAIANLEGNNFNIVVEAFKEWEDP 120
DB 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAAIANLEGNNFNIVVEAFKEWEDP 120

QY 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFEVPLLSVYAAANLHLAIRDVSIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFEVPLLSVYAAANLHLAIRDVSIFGER 180

QY 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNLRDLTLTVL 240
DB 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNLRDLTLTVL 240

QY 241 DIAAFPNYDNRYPYIQPVGQLTRVYTDPLINFNPQLQSVAQLPTFNWESSAIRNPHL 300
DB 241 DIAAFPNYDNRYPYIQPVGQLTRVYTDPLINFNPQLQSVAQLPTFNWESSAIRNPHL 300

QY 301 FDLNNLTFTDWFSGVGRNFGYGHVVISLIGGNTSPIYGREANQPPRSFTFNGPV 360
DB 301 FDLNNLTFTDWFSGVGRNFGYGHVVISLIGGNTSPIYGREANQPPRSFTFNGPV 360

QY 361 FRTLSPITLRLLOQCORHFNLRGEGVEFSTPTNSFTYRGVTGVDLSITELPPEDNSVP 420
DB 361 FRTLSPITLRLLOQWPAPPNLRGVEGEFSTPTNSFTYRGVTGVDLSITELPPEDNSVP 420

QY 421 PREGYSHRLCHATFVQSGTPPLTTGTVFSTWTHRSATLNTIDPERINQIPLVKGFVWG 480
DB 421 PREGYSHRLCHATFVQSGTPPLTTGTVFSTWTHRSATLNTIDPERINQIPLVKGFVWG 480

QY 481 GTSVITGPGTGDDILRRNTFGDVSLOWNINSPIQRLRPRYASSRDARVIVLTGAA 540
DB 481 GTSVITGPGTGDDILRRNTFGDVSLOWNINSPIQRYLRPRYASSRDARVIVLTGAA 540

QY 541 STGVGGQVSNMPLQKTMIEGENTLSTRTYTDSPNPFSPFRANPDIIIGISEQPLFGAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEGENTLSTRTYTDSPNPFSPFRANPDIIIGISEQPLFGAGSI 600

QY 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVDYHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVDYHIDQVSNLV 660

QY 661 DCLSDPFCLEKRELSEKVKHAKRLSDERNLLODPNFRGINQRPDRGWGSTDIITQGGD 720
DB 661 DCLSDPFCLEKRELSEKVKHAKRLSDERNLLODPNFRGINQRPDRGWGSTDIITQGGD 720

QY 721 DVPKENVTLPGTVDCPYLYQKIDESKLYATRYELRGYLEDSDQLEIYLIAVNAKH 780
DB 721 DVPKENVTLPGTVDCPYLYQKIDESKLYATRYELRGYLEDSDQLEIYLIRYNAXH 780

QY 781 EIVNVFGTSLWPLSAQSPIGKGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVFGTSLWPLSAQSPIGKGEPNRCAPHLEWNPDLDCSC 823

US-09-972-175-10
Sequence 10, Application US/09972175
Publication No. US20030101482A1
GENERAL INFORMATION:
APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,175
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/337,635
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-972-175-10

Query Match 98.3%; Score 4283; DB 11; Length 1189;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 813; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MEENNQCIPYCNLSNPEVLLDGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYCNLSNPEVLLDGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60

QY 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAAIANLEGNNFNIVVEAFKEWEDP 120
DB 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAAIANLEGNNFNIVVEAFKEWEDP 120

QY 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFEVPLLSVYAAANLHLAIRDVSIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFEVPLLSVYAAANLHLAIRDVSIFGER 180

QY 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNLRDLTLTVL 240
DB 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGLNLPKSTYQDWITYNLRDLTLTVL 240

QY 241 DIAAFPNYDNRYPYIQPVGQLTRVYTDPLINFNPQLQSVAQLPTFNWESSAIRNPHL 300
DB 241 DIAAFPNYDNRYPYIQPVGQLTRVYTDPLINFNPQLQSVAQLPTFNWESSAIRNPHL 300

QY 301 FDLNNLTFTDWFSGVGRNFGYGHVVISLIGGNTSPIYGREANQPPRSFTFNGPV 360
DB 301 FDLNNLTFTDWFSGVGRNFGYGHVVISLIGGNTSPIYGREANQPPRSFTFNGPV 360

us-09-918-485-2.rapb

Wed Oct 15 11:56:19 2003

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QY 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFTPTNSFTYRGRTVDSLTPELPPDNPV 420
DB 361 FRTLSNPTLRLLQPCWAPPNLRGVEGVEFTPTNSFTYRGRTVDSLTPELPPDNPV 420
QY 421 PREGYSHRLCHATFVQSGTGPFLTTGTVFVSWTHRSATLNTIDPERINQIPLVKGRFVWG 480
DB 421 PREGYSHRLCHATFVQSGTGPFLTTGTVFVSWTHRSATLNTIDPERINQIPLVKGRFVWG 480
QY 481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540
DB 481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540
QY 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600
DB 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
QY 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720
DB 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720
QY 721 DVFKNVTTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSDLEIYLAYNAKH 780
DB 721 DVFKNVTTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSDLEIYLAYNAKH 780
QY 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

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RESULT 7

US-09-972-175-8
; Sequence 8, Application US/09972175
; Publication No. US20030101482A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.
Metzger, Anne-Marie Light

TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/972,175

FILING DATE: 05-Oct-2001

CLASSIFICATION: Unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/337,635

FILING DATE: Unknown

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: MECO.206

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1189 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-972-175-8

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Query Match 98.3%; Score 4282; DB 11; Length 1189;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 812; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 MEENQNCIPYNCNPEVLLDGERISTGNSSIDISLSVQFLVNSVFGGFLVGLI 60

DB 1 MEENQNCIPYNCNPEVLLDGERISTGNSSIDISLSVQFLVNSVFGGFLVGLI 60

QY 61 DFVQGIQVPSQDAFLVQIEQLINERIAEFAARNAALANLEGLGNFNFIYVEAFKEWEDD 120

DB 61 DFVQGIQVPSQDAFLVQIEQLINERIAEFAARNAALANLEGLGNFNFIYVEAFKEWEDD 120

QY 121 NPAATRTVTDRIIDGLLEDRIPSPRISGFVPLLSVYAAANHLAILRDSVIFGER 180

DB 121 NPAATRTVTDRIIDGLLEDRIPSPRISGFVPLLSVYAAANHLAILRDSVIFGER 180

QY 181 WGLTTINNNYNNLRIRHIDEVADHCANTYNGLNLPKSTYODMTYNNLRRLDLTLTVL 240

DB 181 WGLTTINNNYNNLRIRHIDEVADHCANTYNGLNLPKSTYODMTYNNLRRLDLTLTVL 240

QY 241 DIAAFPPYNNRRYPIQVQGLTRVYTDPLINENPOLQSVQALPTFNNMESSAIRNPHL 300

DB 241 DIAAFPPYNNRRYPIQVQGLTRVYTDPLINENPOLQSVQALPTFNNMESSAIRNPHL 300

QY 301 FDIANNLTFTDFSVGRNFYWGHRVSSILIGGNTTSPYIGREANOEPPRSFTFNGPV 360

DB 301 FDIANNLTFTDFSVGRNFYWGHRVSSILIGGNTTSPYIGREANOEPPRSFTFNGPV 360

QY 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFTPTNSFTYRGRTVDSLTPELPPDNPV 420

DB 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFTPTNSFTYRGRTVDSLTPELPPDNPV 420

QY 421 PREGYSHRLCHATFVQSGTGPFLTTGTVFVSWTHRSATLNTIDPERINQIPLVKGRFVWG 480

DB 421 PREGYSHRLCHATFVQSGTGPFLTTGTVFVSWTHRSATLNTIDPERINQIPLVKGRFVWG 480

QY 481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540

DB 481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPITQYRLFRYASSRDARVILVTGAA 540

QY 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600

DB 541 STGVGGQVSNMPLQKMEIGENLTSTRTYTDPSNPFSPRANPDIIIGISQPLFGAGSI 600

QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660

DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660

QY 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720

DB 661 DCLSDFCDEKRELSKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720

QY 721 DVFKNVTTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSDLEIYLAYNAKH 780

DB 721 DVFKNVTTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSDLEIYLAYNAKH 780

QY 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

DB 781 EIVNVPGTGLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 8

US-09-972-175-59
; Sequence 59, Application US/09972175
; Publication No. US20030101482A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

Wed Oct 15 11:56:19 2003

Query Match 98.2%; Score 4281; DB 11; Length 1189;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 813; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNFIYVEAFKEWEDP 120
DB 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNFIYVEAFKEWEDP 120
QY 121 NNPAITRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
DB 121 NNPAITRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
QY 181 WGLTTNNVENYNNLRIRHIDYADHCANTYNNRGLNNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTNNVENYNNLRIRHIDYADHCANTYNNRGLNNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRRIPIQVQGLTREYVTDPLINENPOLQSVQALPTFNWMESSAIRNPHL 300
DB 241 DIAAFFPNYDNRRIPIQVQGLTREYVTDPLINENPOLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPPRSFTFNGPV 360
DB 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPPRSFTFNGPV 360
QY 361 FRTLSIPTLLRLLQPCORHFNLRGGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
DB 361 FRTLSIPTLLRLLQPCORHFNLRGGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPTLTGTVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
DB 421 PREGYSHRLCHATFVQSGTPTLTGTVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDVSQVNSPITQRYRLRYASSRDARVILVTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGDVSQVNSPITQRYRLRYASSRDARVILVTGAA 540
QY 541 STGVGGQVSNMPLQKTMIEIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQPLFAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQPLFAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
QY 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSDTITIOGGD 720
DB 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSDTITIOGGD 720
QY 721 DVPKENYVTLPGTVDECYPTLYYQKIDSKKATRYELRGYIEDSQDLEIYLIYNAKH 780
DB 721 DVPKENYVTLPGTVDECYPTLYYQKIDSKKATRYELRGYIEDSQDLEIYLIYNAKH 780

RESULT 10
US-09-826-660-21
Sequence 21, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven E.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: NA-714XC2D1
CURRENT APPLICATION NUMBER: US/09/826,660

CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 1163
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-21

Query Match 94.3%; Score 4111.5; DB 9; Length 1163;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 787; Conservative 8; Mismatches 23; Indels 5; Gaps 1;
QY 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNONQICIPYNCISNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNFIYVEAFKEWEDP 120
DB 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAIAIANLEGNNFNFIYVEAFKEWEDP 120
QY 121 NNPAITRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
DB 121 NNPAITRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAAQAAHLAILRDSVIFGER 180
QY 181 WGLTTNNVENYNNLRIRHIDYADHCANTYNNRGLNNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTNNVENYNNLRIRHIDYADHCANTYNNRGLNNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRRIPIQVQGLTREYVTDPLINENPOLQSVQALPTFNWMESSAIRNPHL 300
DB 241 DIAAFFPNYDNRRIPIQVQGLTREYVTDPLINENPOLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPPRSFTFNGPV 360
DB 301 FDIILNNLTFTDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQPPRSFTFNGPV 360
QY 361 FRTLSIPTLLRLLQPCORHFNLRGGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
DB 361 FRTLSIPTLLRLLQPCORHFNLRGGEGVEFSTPTNSFTYGRGTVDLSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPTLTGTVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
DB 421 PREGYSHRLCHATFVQSGTPTLTGTVFSWTHRSATLNTIDPERINQIPLVKGRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDVSQVNSPITQRYRLRYASSRDARVILVTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGDVSQVNSPITQRYRLRYASSRDARVILVTGAA 540
QY 541 STGVGGQVSNMPLQKTMIEIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQPLFAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEIGENLTSTRTFYTDPSNPFSSFRANPDIIIGISEQPLFAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQAVNALFTSSNQIGLKTVDVTHIDQVSNLV 660
QY 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSDTITIOGGD 720
DB 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINQPDGRWGSDTITIOGGD 720
QY 721 DVPKENYVTLPGTVDECYPTLYYQKIDSKKATRYELRGYIEDSQDLEIYLIYNAKH 780
DB 721 DVPKENYVTLPGTVDECYPTLYYQKIDSKKATRYELRGYIEDSQDLEIYLIYNAKH 780

QY 781 EIVNPTGSLWPLSAQSPGKCEPNRCAPHLEWNPDLDCSC 823
Db 781 ETVNPTGSLWPLSAQSPGKCAHSH-----HFSLDIDVGC 818

RESULT 11

US-09-873-873-30
; Sequence 30, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-30

Query Match 70.9%; Score 3088; DB 9; Length 1193;
Best Local Similarity 71.8%; Pred. No. 2.4e-283;
Matches 606; Conservative 68; Mismatches 132; Indels 38; Gaps 12;
QY 1 MEEN-NQOQIPYCNLSNPEEVLDDGERISTGSSIDISLSVQFLVSNFVPGGFLVGL 59
Db 1 MDNNINECIPYCNLSNPEEVLDDGERISTGSSIDISLSVQFLVSNFVPGGFLVGL 60
QY 60 IDPVMGIVGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 119
Db 61 VDIWIGIFGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 120
QY 120 PNNPATRTRVIDRFRILDGLLERDIPSRISGFEVPLLSVYQAANLHLAIRDSVIFGE 179
Db 121 PTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAANLHLVLRDVSFVQ 180
QY 180 RWGLTTINVENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTV 239
Db 181 RWGFDAAATINSRYNDLTRIGNYTDYAVRWYNTGLERVMGPDSDRWRYNQFRRLTLTV 240
QY 240 LDIAAFENYDNRYPYIQPVQGLTFEVDPLI-NFNQLQSVQALPTFNWMESSAIRNP 298
Db 241 LDIALVFPNDSRRYPIRTVQSLTREIYNPNVLENFDGSRGSAQ-----GIERS-IRSP 294
QY 299 HLFIDILNLTFTDWPFSGRNFYWGHRVSISSIG--GNNITSPYIGREANQEPFRSFT- 355
Db 295 HLMDILNSITITD--AHRGYYSWGCHQIMASPVGSGPEFTFPLYGTMNAAPQORIVA 352
QY 356 -FNGPVFRILSTPLRLLOQPCORHHFN-----LRGEGVEFSTPTN-----SFTYGR 403
Db 353 QLGGQGYRTLS-----STLYRRPFNIGINNQLSLVLDGTEFAYGTSSNLPASVYRKS 404
QY 404 GTVDSLTLPBENSVPREGYSHRLCHATFVORSGTPELTITGVV-----FSWTHRSATLT 459
Db 405 GTVDSLDEIPPNQNNVPPQGGSHRLSHVSMF-RSGFSNNSVSIIRAPFWSHRSATLT 463
QY 460 NTIDPERINQIPLVKGFRVWGTSVITGPGFTGGDILRRNTFGDFVSLQVWINSPIITORY 519
Db 464 NTIDPERINQIPLVKGFRVWGTSVITGPGFTGGDILRRNTFGDFVSLQVWINSPIITORY 523
QY 520 RLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMWEGENLTSTRTFRYTDPSNPFS 579

Db 524 RLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMWEGENLTSTRTFRYTDPSNPFS 583
QY 580 FRANPDIIGISBQPLFGAGSISGELYIDKIEIILADATFEAESDLERAKAVNALFTSS 639
Db 584 FRANPDIIGISBQPLFGAGSISGELYIDKIEIILADATFEAESDLERAKAVNALFTSS 643
QY 640 NOIGLKTDTYHIDQVSNLVCLSDFCLEKRELSKVGIAKRLSDERNLLQDNFRG 699
Db 644 NOIGLKTDTYHIDQVSNLVCLSDFCLEKRELSKVGIAKRLSDERNLLQDNFRG 703
QY 700 INRPDRGRGSTDITIQGDDVPFKNYVTLTGTVDECYPTLYYQKIDSKLKAYTRYEL 759
Db 704 INRPDRGRGSTDITIQGDDVPFKNYVTLTGTVDECYPTLYYQKIDSKLKAYTRYEL 763
QY 760 RYVIEDSQLEIYLAYNAKHEIVNVPVGTSLWPLSAQSPGKCEPNRCAPHLEWNPDL 819
Db 764 RYVIEDSQLEIYLAYNAKHEIVNVPVGTSLWPLSAQSPGKCEPNRCAPHLEWNPDL 823
QY 820 DCSC 823
Db 824 DCSC 827

RESULT 12

US-09-997-914-30
; Sequence 30, Application US/09997914
; Publication No. US20030119158A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad Spectrum d-Endotoxins
; FILE REFERENCE: 11792.0215.DVUS01 MECO:215--1
; CURRENT APPLICATION NUMBER: US/09/997,914
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/261,040
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-997-914-30

Query Match 70.9%; Score 3088; DB 11; Length 1193;
Best Local Similarity 71.8%; Pred. No. 2.4e-283;
Matches 606; Conservative 68; Mismatches 132; Indels 38; Gaps 12;
QY 1 MEEN-NQOQIPYCNLSNPEEVLDDGERISTGSSIDISLSVQFLVSNFVPGGFLVGL 59
Db 1 MDNNINECIPYCNLSNPEEVLDDGERISTGSSIDISLSVQFLVSNFVPGGFLVGL 60
QY 60 IDPVMGIVGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 119
Db 61 VDIWIGIFGPSOWDAFLVQIQLINERIAEFARNAANLEGLGNFNLYVEAFKEWEED 120
QY 120 PNNPATRTRVIDRFRILDGLLERDIPSRISGFEVPLLSVYQAANLHLAIRDSVIFGE 179
Db 121 PTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAANLHLVLRDVSFVQ 180
QY 180 RWGLTTINVENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTV 239
Db 181 RWGFDAAATINSRYNDLTRIGNYTDYAVRWYNTGLERVMGPDSDRWRYNQFRRLTLTV 240
QY 240 LDIAAFENYDNRYPYIQPVQGLTFEVDPLI-NFNQLQSVQALPTFNWMESSAIRNP 298
Db 241 LDIALVFPNDSRRYPIRTVQSLTREIYNPNVLENFDGSRGSAQ-----GIERS-IRSP 294

Wed Oct 15 11:56:19 2003

QY	299	HLFDILNNLTFTDWFSGVRNFWGHRVVISLIG--CGNITSPYIGREANQPPRSFT-	355
Db	295	HLMDILNLTFTDWFSGVRNFWGHRVVISLIG--CGNITSPYIGREANQPPRSFT-	352
QY	356	FNGPVFRTLSPTLRLLQPCORHFN-----LRGGEVFEFTPTN-----SFTYRGR	403
Db	353	QLGQGVYRTLS-----STLYRRPFNIGINNQQLSVLDTGEFAYGSSNLPNAVYRKS	404
QY	404	GTVDLSLTPEDNSVPPREGYSHRLCHATFVQSGTPTFTTGV-----FSWTHRSATLT	459
Db	405	GTVDLSLTPEDNSVPPREGYSHRLCHATFVQSGTPTFTTGV-----FSWTHRSATLT	463
QY	460	NTIDPERINQIPLVKGFRVWGTSVITGPGTGGDILRRNTFGDFVSLQVINSPIQRY	519
Db	464	NTIDPERINQIPLVKGFRVWGTSVITGPGTGGDILRRNTFGDFVSLQVINSPIQRY	523
QY	520	RLRFRYASSRDARVILTGAASCTGCGVSVNMPLQKTMELGENLTSRFRYTFDSNPF	579
Db	524	RLRFRYASSRDARVILTGAASCTGCGVSVNMPLQKTMELGENLTSRFRYTFDSNPF	583
QY	580	FRANPDIIGISEQPLFGAGSISSGELYIDKIELIILADATFEASDLERAKAVNALFTSS	639
Db	584	FRANPDIIGISEQPLFGAGSISSGELYIDKIELIILADATFEASDLERAKAVNALFTSS	643
QY	640	NOIGLKTVDYHIDQVSNLVDCLDEKRELSKVKHAKRLSDERNLLQDPNFRG	699
Db	644	NOIGLKTVDYHIDQVSNLVDCLDEKRELSKVKHAKRLSDERNLLQDPNFRG	703
QY	700	INRQDRGWRGSDTITIQGDDVFKENYVTLPGTVDCEYPTLYQKIDSKLKAYTRYEL	759
Db	704	INRQDRGWRGSDTITIQGDDVFKENYVTLPGTVDCEYPTLYQKIDSKLKAYTRYEL	763
QY	760	RGYIEDSQLEIYLIRYNAKHEIIVNVFGTSLMPLSAQSPGKCGEPCNRCAPHLWNPD	819
Db	764	RGYIEDSQLEIYLIRYNAKHEIIVNVFGTSLMPLSAQSPGKCGEPCNRCAPHLWNPD	823
QY	820	DCSC 823	
Db	824	DCSC 827	
RESULT 14			
US-09-873-873-10			
; Sequence 30, Application US/09873873			
; Patent No. US20020064865A1			
; GENERAL INFORMATION:			
; APPLICANT: Malvar, Thomas			
; APPLICANT: Gilmer, Amy Jelen			
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins			
; FILE REFERENCE: MECO:210--2			
; CURRENT APPLICATION NUMBER: US/09/873,873			
Query Match 70.9%; Score 3088; DB 12; Length 1193;			
Best Local Similarity 71.8%; Pred. No. 2.4e-283;			

Matches 606; Conservative 68; Mismatches 132; Indels 38; Gaps 12;

us-09-918-485-2.rapb

Wed Oct 15 11:56:19 2003

Db	464	NTIDPERITQIELVKAHTLQSGTTVVRGFTGGDIURRTSGGPFYATVIVNINQQLPQRY	523
Qy	520	RLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMETGENLTSRTFRYTDPSNPF5	579
Db	524	RARIRYASTTNLRIVV-TVAGERIFAGQ-----FNKMTDGTGDLTTFQSFYATINTAFT	576
Qy	580	FRANPDIIIGISBQPLFGAGSISG-ELYIDKIEIILADATFEASDLERAQKAVNALFTS	638
Db	577	FPMQSQSFTV-----GADTFSCGNEVYIDREFELIPVTATFEAYDLERAQKAVNALFTS	630
Qy	639	SNOIGLKTVDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKLSDERNLLQDPNFR	698
Db	631	INQIGIKTDYHIDQVSNLVDCLSEFCLDEKRELSKVKHAKLSDERNLLQDPNFK	690
Qy	699	GINQPDGRGSGTDITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDESKLKAYTRYE	758
Db	691	GINQLDRGWRGSGTDITIQRGDDVFKENYVTLPGTFDECYPTLYQKIDESKLKAFTRYQ	750
Qy	759	LRGVIEDSQBLEIYLIRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNP	818
Db	751	LRGVIEDSQBLEIYLIRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNP	810
Qy	819	LDCSC	823
Db	811	LDCSC	815

Search completed: October 9, 2003, 13:36:15
Job time : 80 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 04:02:39 ; Search time 232 Seconds
(without alignments)
5157.714 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711
Sequence: 1 AGCTTCAATAGACTTCAA.....GATCTAGATTGTCCTGCAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2711	100.0	2711	1 US-08-461-551-1	Sequence 1, Appli
2	2711	100.0	2711	4 US-09-037-621A-1	Sequence 1, Appli
3	2664	98.3	3923	3 US-08-465-609-4	Sequence 4, Appli
4	2659.2	98.1	3923	3 US-09-176-320-7	Sequence 7, Appli
5	2431	89.7	3567	1 US-08-602-737-1	Sequence 1, Appli
6	2431	89.7	3567	3 US-09-001-982-1	Sequence 1, Appli
7	2429.4	89.6	3567	1 US-07-828-788A-15	Sequence 15, Appl
8	2429.4	89.6	3567	1 US-08-356-034-5	Sequence 5, Appli
9	2429.4	89.6	3567	2 US-08-980-071-1	Sequence 1, Appli
10	2429.4	89.6	3567	2 US-08-980-071-11	Sequence 11, Appl
11	2429.4	89.6	3567	2 US-08-757-536-1	Sequence 1, Appli
12	2429.4	89.6	3567	2 US-08-757-536-11	Sequence 11, Appl
13	2429.4	89.6	3567	3 US-09-314-093-1	Sequence 1, Appli
14	2429.4	89.6	3567	3 US-09-314-093-11	Sequence 11, Appl
15	2429.4	89.6	3567	3 US-08-933-891-5	Sequence 5, Appli
16	2429.4	89.6	3567	3 US-09-250-848-1	Sequence 1, Appli
17	2429.4	89.6	3567	3 US-09-250-848-11	Sequence 11, Appl
18	2429.4	89.6	3567	3 US-09-251-885-1	Sequence 1, Appli
19	2429.4	89.6	3567	3 US-09-251-885-11	Sequence 11, Appl
20	2429.4	89.6	3567	4 US-09-337-635-1	Sequence 1, Appli
21	2429.4	89.6	3567	4 US-09-337-635-11	Sequence 11, Appl
22	2429.4	89.6	3567	4 US-09-337-280-1	Sequence 1, Appli
23	2429.4	89.6	3567	4 US-09-337-280-11	Sequence 11, Appl
24	2429.4	89.6	3567	4 US-09-521-344-5	Sequence 5, Appli
25	2429.4	89.6	3567	5 PCT-US92-11337-15	Sequence 15, Appl
26	2429.4	89.6	3567	6 5188960-5	Patent No. 5188960
27	2427.8	89.6	3567	2 US-08-980-071-3	Sequence 3, Appli

28	2427.8	89.6	3567	2 US-08-980-071-5	Sequence 5, Appli
29	2427.8	89.6	3567	2 US-08-980-071-9	Sequence 9, Appli
30	2427.8	89.6	3567	2 US-08-757-536-3	Sequence 3, Appli
31	2427.8	89.6	3567	2 US-08-757-536-5	Sequence 5, Appli
32	2427.8	89.6	3567	2 US-08-757-536-9	Sequence 9, Appli
33	2427.8	89.6	3567	3 US-09-314-093-3	Sequence 3, Appli
34	2427.8	89.6	3567	3 US-09-314-093-5	Sequence 5, Appli
35	2427.8	89.6	3567	3 US-09-314-093-9	Sequence 9, Appli
36	2427.8	89.6	3567	3 US-09-250-848-5	Sequence 5, Appli
37	2427.8	89.6	3567	3 US-09-250-848-9	Sequence 9, Appli
38	2427.8	89.6	3567	3 US-09-250-848-9	Sequence 9, Appli
39	2427.8	89.6	3567	3 US-09-251-885-3	Sequence 3, Appli
40	2427.8	89.6	3567	3 US-09-251-885-5	Sequence 5, Appli
41	2427.8	89.6	3567	3 US-09-251-885-9	Sequence 9, Appli
42	2427.8	89.6	3567	4 US-09-337-635-3	Sequence 3, Appli
43	2427.8	89.6	3567	4 US-09-337-635-5	Sequence 5, Appli
44	2427.8	89.6	3567	4 US-09-337-635-9	Sequence 9, Appli
45	2427.8	89.6	3567	4 US-09-337-280-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-461-551-1
; Sequence 1, Application US/08461551
; Patent No. 5792928
; GENERAL INFORMATION:
; APPLICANT: SANCHIS, Vincent
; APPLICANT: LERRECLUS, Didier
; APPLICANT: MENOU, Ghislaine
; APPLICANT: LECADET, Marguerite-Marie
; APPLICANT: MARTOURET, Daniel
; APPLICANT: DEODONER, Raymond
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
; TITLE OF INVENTION: POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:									
SEQUENCE CHARACTERISTICS:									
LENGTH: 2711 base pairs									
TYPE: nucleic acid									
STRANDEDNESS: single									
TOPOLOGY: linear									
MOLECULE TYPE: DNA (genomic)									
US-08-461-551-1									
Query Match 100.0%; Score 2711; DB 1; Length 2711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AAGCTTCAATAGAACTCTCAAACTCTCGATGACTGCTTACTCTTTTAAATAGTCTCTACTTG	60						
Db	1	AAGCTTCAATAGAACTCTCAAACTCTCGATGACTGCTTACTCTTTTAAATAGTCTCTACTTG	60						
Qy	61	ACAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCGATATATCGATATTTTATAA	120						
Db	61	ACAGGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCGATATATCGATATTTTATAA	120						
Qy	121	AATTTGTAGCTTTTGTATTTTTCATAAGATGTGTCAATGTATTAATTCGTTGTA	180						
Db	121	AATTTGTAGCTTTTGTATTTTTCATAAGATGTGTCAATGTATTAATTCGTTGTA	180						
Qy	181	TGAARAACAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAATAAATAAATAAATAA	240						
Db	181	TGAARAACAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAATAAATAAATAAATAA	240						
Qy	241	ATGAGGAAATTAATCAAACTATCAGAACTTTTGTAGTTTAAATAAATAAATAAATAAATAA	300						
Db	241	ATGAGGAAATTAATCAAACTATCAGAACTTTTGTAGTTTAAATAAATAAATAAATAAATAA	300						
Qy	301	GTACTTTTGTAGTGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGAATAATA	360						
Db	301	GTACTTTTGTAGTGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGAATAATA	360						
Qy	361	CTTGTTCAGTTTCTGATATCTAATCTTGTACAGGGGAGGAGATTTTGTAGTGAATAATA	420						
Db	361	CTTGTTCAGTTTCTGATATCTAATCTTGTACAGGGGAGGAGATTTTGTAGTGAATAATA	420						
Qy	421	GATTTTGTATGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGAATAATA	480						
Db	421	GATTTTGTATGGGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGAATAATA	480						
Qy	481	CAATTAATTAATGAAAGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGAATAATA	540						
Db	481	CAATTAATTAATGAAAGAAATAGTGGGCTTCTCAATGGGATGCAATTTAGTGAATAATA	540						
Qy	541	GGATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAAGATCT	600						
Db	541	GGATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAAGATCT	600						
Qy	601	AATATCCAGCAACCCAGGACAGATTAATTCATCGCTTTTGTATATCTTGTATGAGTCTT	660						
Db	601	AATATCCAGCAACCCAGGACAGATTAATTCATCGCTTTTGTATATCTTGTATGAGTCTT	660						
Qy	661	GAAAGGCAATCTTCTGATTTTCAATTTTGTATATCTTGTATATCTTGTATGAGTCTT	720						
Db	661	GAAAGGCAATCTTCTGATTTTCAATTTTGTATATCTTGTATATCTTGTATGAGTCTT	720						
Qy	721	GCTCAAGCGGCAATCTGATCTGATATATATGATATATGATATGATATGATATGATATGAT	780						
Db	721	GCTCAAGCGGCAATCTGATCTGATATATGATATATGATATGATATGATATGATATGAT	780						
Qy	781	TTGGGATGACAAAGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT	840						
Db	781	TTGGGATGACAAAGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT	840						
Qy	841	GAATATGCTGATCACTGTGCAAAATAGTGAATATGATATGATATGATATGATATGATATGAT	900						
Db	841	GAATATGCTGATCACTGTGCAAAATAGTGAATATGATATGATATGATATGATATGATATGAT	900						

Qy	901	ACGTATCAAGATTGGATAACATATTAATCGATTACGGAGAGACTTAACAAATGACTGTATTATA	960						
Db	901	ACGTATCAAGATTGGATAACATATTAATCGATTACGGAGAGACTTAACAAATGACTGTATTATA	960						
Qy	961	GATATCGCGCTTCTTCTTCCAAATATGCAATAGGAGATATCCAAATAGCCAGTTGGT	1020						
Db	961	GATATCGCGCTTCTTCTTCCAAATATGCAATAGGAGATATCCAAATAGCCAGTTGGT	1020						
Qy	1021	CAACTAACAGGGAAGTTTATACGGACCAATTAATTAATTTTAAATCCACAGTTACAGTCT	1080						
Db	1021	CAACTAACAGGGAAGTTTATACGGACCAATTAATTAATTTTAAATCCACAGTTACAGTCT	1080						
Qy	1081	GTAGCTCAATTAACCTTATACCTTTATGAGAGAGAGCAATAGAAATCTCTCAATTTA	1140						
Db	1081	GTAGCTCAATTAACCTTATACCTTTATGAGAGAGAGCAATAGAAATCTCTCAATTTA	1140						
Qy	1141	TTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1200						
Db	1141	TTTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1200						
Qy	1201	TATGGGAGGAGCATCGAGTATATAGCTTATAGGAGTGTAAACATACATCTCT	1260						
Db	1201	TATGGGAGGAGCATCGAGTATATAGCTTATAGGAGTGTAAACATACATCTCT	1260						
Qy	1261	ATATATGGAAGAGGCGGAAACAGAGAGCTTCAAGATCTTTTAAATGAGCCGGTA	1320						
Db	1261	ATATATGGAAGAGGCGGAAACAGAGAGCTTCAAGATCTTTTAAATGAGCCGGTA	1320						
Qy	1321	TTTAGGACTTTATCAATTTCTTACTTTTACAGCAACCTTTCAGAGCGGCAACAT	1380						
Db	1321	TTTAGGACTTTATCAATTTCTTACTTTTACAGCAACCTTTCAGAGCGGCAACAT	1380						
Qy	1381	TTTAAATTAACGTGTGTGTGAGGAGTAGAATTTTCTACACTACAAATAGCTTTACGTAT	1440						
Db	1381	TTTAAATTAACGTGTGTGTGAGGAGTAGAATTTTCTACACTACAAATAGCTTTACGTAT	1440						
Qy	1441	GCAGAGAGGAGTACCGTTGATTTCTTAACTGAAATACCGCTGAGGATTAATAGTGGCA	1500						
Db	1441	GCAGAGAGGAGTACCGTTGATTTCTTAACTGAAATACCGCTGAGGATTAATAGTGGCA	1500						
Qy	1501	CCTCGGAGGAGATAGTCACTGTTTATGTCACTGAACTTTTGTTCAGGAGATCTCGAACA	1560						
Db	1501	CCTCGGAGGAGATAGTCACTGTTTATGTCACTGAACTTTTGTTCAGGAGATCTCGAACA	1560						
Qy	1561	CTTTTAACTGAGTGTAGTATTTCTTGGACGCACTGTAGTGAACCTTTAGAGTTTGGGG	1620						
Db	1561	CTTTTAACTGAGTGTAGTATTTCTTGGACGCACTGTAGTGAACCTTTAGAGTTTGGGG	1620						
Qy	1621	ACAAATGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTGGGG	1680						
Db	1621	ACAAATGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGGATTTAGAGTTTGGGG	1680						
Qy	1681	GGCACTCTGTCTTACAGGAGGAGTATACAGGAGGAGATATCTTCGAGAGAAATACC	1740						
Db	1681	GGCACTCTGTCTTACAGGAGGAGTATACAGGAGGAGATATCTTCGAGAGAAATACC	1740						
Qy	1741	TTTGGTGAATTTGATCTCTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800						
Db	1741	TTTGGTGAATTTGATCTCTCAAGTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800						
Qy	1801	TTAAGATTTCTGTTACGCTTCCAGTAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT	1860						
Db	1801	TTAAGATTTCTGTTACGCTTCCAGTAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT	1860						
Qy	1861	TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT	1920						
Db	1861	TCCACAGAGTGGGAGGCGCAAGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT	1920						
Qy	1921	GGGAGAGAACTTAACATCTAGAACTTTAGATATACCGATTTTGTAGTGTAGTGTAGTGTAGT	1980						
Db	1921	GGGAGAGAACTTAACATCTAGAACTTTAGATATACCGATTTTGTAGTGTAGTGTAGTGTAGT	1980						
Qy	1981	AGAGCTAATCCAGATATTAATTCGGATAAGTGAACACCTCTATTTGGTGTGAGGTTCTATT	2040						

1981 AGAGCTAAATCCAGATATAATTTGGATAAGTGAACAAACCTCTATTTGGTCAGGTTCTATT 2040
2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
2101 GCAGATCTGATTTGAAGAGAGACAAAGAGCGGCTGAATGCCCTGTTTACTTCTTCCAAAT 2160
2101 GCAGATCTGATTTGAAGAGAGACAAAGAGCGGCTGAATGCCCTGTTTACTTCTTCCAAAT 2160
2161 CAATCGGGTTAAACCCGATGACGGATATATATTTGATCAATTTAGT 2220
2161 CAATCGGGTTAAACCCGATGACGGATATATATTTGATCAATTTAGT 2220
2221 GATTGTTTATCAGATGAATTTTCTGATGAAAGCGAGAAATTTGCGAGAAAGTCAAA 2280
2221 GATTGTTTATCAGATGAATTTTCTGATGAAAGCGAGAAATTTGCGAGAAAGTCAAA 2280
2281 CATGGAAGCGACTAGTGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATC 2340
2281 CATGGAAGCGACTAGTGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATC 2340
2341 AATAGACAACACCGCTGGCTGGAGAGGAGTACAGATATTACCATCCAGAGGAGAT 2400
2341 AATAGACAACACCGCTGGCTGGAGAGGAGTACAGATATTACCATCCAGAGGAGAT 2400
2401 GAGCTATTCAAGAGAAATTTACGTACACTACCGGGTACCGTTGATGAGTGCTATCCACG 2460
2401 GAGCTATTCAAGAGAAATTTACGTACACTACCGGGTACCGTTGATGAGTGCTATCCACG 2460
2461 TATTTATATCAGAAATAGATGAGTCAAGTCAAAATTTAAAGCTTATACCGTTTATGAATTAAGA 2520
2461 TATTTATATCAGAAATAGATGAGTCAAGTCAAAATTTAAAGCTTATACCGTTTATGAATTAAGA 2520
2521 GGGTATATCGAAGATGATCAAGCTTAGAATTTAGAAATTTATTTGATCGCGTACAAACAC 2580
2521 GGGTATATCGAAGATGATCAAGCTTAGAATTTAGAAATTTATTTGATCGCGTACAAACAC 2580
2581 GAAATAGTAAATGTGCGAGCGGTTCTTATGCGCGCTTTCAGCCCAAAAGTCCCAATC 2640
2581 GAAATAGTAAATGTGCGAGCGGTTCTTATGCGCGCTTTCAGCCCAAAAGTCCCAATC 2640
2641 GGAAGTGTGGAAACCGAATCGATGCGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
2641 GGAAGTGTGGAAACCGAATCGATGCGCGCACACCTTTGAATGGAATCCTGATCTAGAT 2700
2701 TGTTCCTGCAG 2711
2701 TGTTCCTGCAG 2711

RESULT 2
US-09-037-621A-1
Sequence 1, Application US/09037621A
Patent No. 6310035
GENERAL INFORMATION:
APPLICANT: SANCHIS, Vincent
LERECIUS, Didier
MENOUE, Ghislaine
LECADET, Marguerite-Marie
MARTOURET, Daniel
DEBONDER, Raymond
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR
POLYPEPTIDES ENDOWED WITH A LARVICIDAL ACTIVITY TOWARDS
LEPIDOPTERA
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
City: Alexandria
STATE: Virginia
COUNTRY: USA

ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,621A
FILING DATE: 10-Mar-1998
CLASSIFICATION: <Unknown>
11-DEC-1989
06-MAY-1988
10-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,551
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/459,754
FILING DATE: 11-DEC-1989
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-037-621A-1
Query Match 100.0%; Score 2711; DB 4; Length 2711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTCAATAGAATCTCAAAATCTCGATGACTGCTTAGTCTTTTAAATACCTGCTACTTG 60
DB 1 AAGCTTCAATAGAATCTCAAAATCTCGATGACTGCTTAGTCTTTTAAATACCTGCTACTTG 60
QY 61 ACAGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCATATATTGATATTTTATAA 120
DB 61 ACAGGGTAGGAACATAATCGGTCAATTTTAAATATGGGCATATATTGATATTTTATAA 120
QY 121 AATTTGTACGTTTTTGTATTTTTCATAGATGTCATATGTTTAAATCGTGTAA 180
DB 121 AATTTGTACGTTTTTGTATTTTTCATAGATGTCATATGTTTAAATCGTGTAA 180
QY 181 TGAATAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAGGAGGTATTTT 240
DB 181 TGAATAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAGGAGGTATTTT 240
QY 241 ATGGAGGAAATAATCAAAATCAATGTCATACCTTCAATGTTTAAAGTAATCCTGAAGAA 300
DB 241 ATGGAGGAAATAATCAAAATCAATGTCATACCTTCAATGTTTAAAGTAATCCTGAAGAA 300
QY 301 GTACTTTGGATGGAGACGATATCAACTGGTAATTAATGATATTTCTCTGCA 360
DB 301 GTACTTTGGATGGAGACGATATCAACTGGTAATTAATGATATTTCTCTGCA 360
QY 361 CTGTTTCAAGTTTCTGGTATCTAACTTTCTACAGGGGAGGATTTTGTAGTTGATTAATA 420
DB 361 CTGTTTCAAGTTTCTGGTATCTAACTTTCTACAGGGGAGGATTTTGTAGTTGATTAATA 420
QY 421 GATTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480

Db	421	GAATTTGATAGGGGAATAGTTGGCCCTTCTCAATCGGATCGCATTTCTAGTACAAATTTGAA	480	1561	CCTTTTTTAAACAACCTGGTGTAGTATTTCTTTGGAACGATCGTGTAGTGCMACTCTTACAAAT	1620
Qy	481	CAATTAATTAATGAAAGATAGCTGAATTTGCTAGGAATCGTCTATTTGCTAAATTTAGAA	540	1561	CCTTTTTTAAACAACCTGGTGTAGTATTTCTTTGGAACGATCGTGTAGTGCMACTCTTACAAAT	1620
Db	481	CAATTAATTAATGAAAGATAGCTGAATTTGCTAGGAATCGTCTATTTGCTAAATTTAGAA	540	1621	ACAAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGTTTGTAGTTGGGG	1680
Qy	541	GGATTAGGAAACAATTTCAATATATATATGTTGGAGCATTTAAAGATGGGAGAGATCCT	600	1621	ACAAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGTTTGTAGTTGGGG	1680
Db	541	GGATTAGGAAACAATTTCAATATATATATGTTGGAGCATTTAAAGATGGGAGAGATCCT	600	1681	GGCACCTCTGTCTATTACAGGACAGAGTTTACAGGAGGGGATATCTTTGGAAGAAATACC	1740
Qy	601	AATAATCCAGCAACACAGACAGAGTAATTTGATCGCTTTGCTATATCTTGAATGGCTACTT	660	1681	GGCACCTCTGTCTATTACAGGACAGAGTTTACAGGAGGGGATATCTTTGGAAGAAATACC	1740
Db	601	AATAATCCAGCAACACAGACAGAGTAATTTGATCGCTTTGCTATATCTTGAATGGCTACTT	660	1741	TTTGGTGAATTTTGTATCTCTACAACTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Qy	661	GAAGGGACATTCCTTCCTTTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATTCGGTTAT	720	1741	TTTGGTGAATTTTGTATCTCTACAACTCAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Db	661	GAAGGGACATTCCTTCCTTTTTCGAAATTTCTGGATTTGAAGTACCCCTTTTATTCGGTTAT	720	1801	TTAAGATTTTCCTTACGCTTCCAGTAGGATCGACAGTTATATAGTATTAACAGGAGCGGCA	1860
Qy	721	GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTCCTGTAATTTTGGAGAAAGA	780	1801	TTAAGATTTTCCTTACGCTTCCAGTAGGATCGACAGTTATATAGTATTAACAGGAGCGGCA	1860
Db	721	GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTCCTGTAATTTTGGAGAAAGA	780	1861	TCCAAGAGTGGGAGCGGCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA	1920
Qy	781	TTGGGATTGACACGATAAATGTCATGAAACTATATAGACTTAATAGGATATTGAT	840	1861	TCCAAGAGTGGGAGCGGCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA	1920
Db	781	TTGGGATTGACACGATAAATGTCATGAAACTATATAGACTTAATAGGATATTGAT	840	1921	GGGGAGACTTAACATCTAGAACATTTAGATATACCGATTTTGTAGTAATCTTTTCAATTT	1980
Qy	841	GAATATCGCTGACCTGTCGAATACGTAATCGTATTAATCGGGATTAATTAATTTACGAAATCT	900	1921	GGGGAGACTTAACATCTAGAACATTTAGATATACCGATTTTGTAGTAATCTTTTCAATTT	1980
Db	841	GAATATCGCTGACCTGTCGAATACGTAATCGTATTAATCGGGATTAATTAATTTACGAAATCT	900	1981	AGAGCTTAATCCAGATATAAATTTGGGATAGTGAACAACTCTATTTGGTGGAGTTCTATT	2040
Qy	901	ACGTATCAAGATTGGATACATATTAATCGATTAACGAGAGACTTAACATTTGACTGTATTA	960	1981	AGAGCTTAATCCAGATATAAATTTGGGATAGTGAACAACTCTATTTGGTGGAGTTCTATT	2040
Db	901	ACGTATCAAGATTGGATACATATTAATCGATTAACGAGAGACTTAACATTTGACTGTATTA	960	2041	AGTAGCGTTTGAACITTTATATAGATAAATTTGAATTTTCTAGCAGATCAACATTTGAA	2100
Qy	961	GATATCGCGCTTCTTTCCAACTATGACATAGAGATTCCTCAATTCAGCAGCTGCT	1020	2041	AGTAGCGTTTGAACITTTATATAGATAAATTTGAATTTTCTAGCAGATCAACATTTGAA	2100
Db	961	GATATCGCGCTTCTTTCCAACTATGACATAGAGATTCCTCAATTCAGCAGCTGCT	1020	2101	GCAGAACTCTGATTTAGAAAGAGCACAAAAGCGGCTGAATGCGCTTTTACTTTCTCCAAAT	2160
Qy	1021	CAACTAAACAGGAGAGTTTATACGGACCCATTAATTTTATCAAGTTTCAAGTCAAGTCT	1080	2101	GCAGAACTCTGATTTAGAAAGAGCACAAAAGCGGCTGAATGCGCTTTTACTTTCTCCAAAT	2160
Db	1021	CAACTAAACAGGAGAGTTTATACGGACCCATTAATTTTATCAAGTTTCAAGTCAAGTCT	1080	2161	CAAAATCGGGTTAAAAACCGATGTGACGGATTTATATTTGATCAAGTATCCAAATTTAGTG	2220
Qy	1081	GTAGCTCAATTTACTACTTTTAAACGTTATGAGAGAGCGGCAATTTAGAAATCTCTATTA	1140	2161	CAAAATCGGGTTAAAAACCGATGTGACGGATTTATATTTGATCAAGTATCCAAATTTAGTG	2220
Db	1081	GTAGCTCAATTTACTACTTTTAAACGTTATGAGAGAGCGGCAATTTAGAAATCTCTATTA	1140	2221	GATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAGAGTCAAA	2280
Qy	1141	TTTGATATATTGATTAATCTTTTAAACGTTATGAGAGAGCGGCAATTTAGAAATCTCTATTA	1200	2221	GATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATTTGTCGAGAGAGTCAAA	2280
Db	1141	TTTGATATATTGATTAATCTTTTAAACGTTATGAGAGAGCGGCAATTTAGAAATCTCTATTA	1200	2281	CATCGAAGCGACTCAGTGTAGCGGAATTTACTTTCAAGATCCAAATTTCAAGAGGATC	2340
Qy	1201	TATTTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGTGTAACATCTCTCT	1260	2281	CATCGAAGCGACTCAGTGTAGCGGAATTTACTTTCAAGATCCAAATTTCAAGAGGATC	2340
Db	1201	TATTTGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGTGTGTAACATCTCTCTCT	1260	2341	AAATAGAACACAGCCGCTGCTGAGAGAGTACAGATATTTACATCCCAAGGAGAGAT	2400
Qy	1261	ATATATGGAAGAGGCGAACACAGGAGCTCCAAAGATCTTTTACTTTTAAATGGACCGGTA	1320	2341	AAATAGAACACAGCCGCTGCTGAGAGAGTACAGATATTTACATCCCAAGGAGAGAT	2400
Db	1261	ATATATGGAAGAGGCGAACACAGGAGCTCCAAAGATCTTTTACTTTTAAATGGACCGGTA	1320	2401	GACGTATTCAAAGAGAAATTTAGTGTACACTACCGGTTACGTTGATGATGCTATCCAAAG	2460
Qy	1321	TTTGAAGCTTTTCAATTTCTTACTTTTACGATTTATTAAGCAACCTTTGCGAGCGCAACAT	1380	2401	GACGTATTCAAAGAGAAATTTAGTGTACACTACCGGTTACGTTGATGATGCTATCCAAAG	2460
Db	1321	TTTGAAGCTTTTCAATTTCTTACTTTTACGATTTATTAAGCAACCTTTGCGAGCGCAACAT	1380	2461	TATTTATATCAGAAAAATAGATGAGTCCGAATTTAAAGCTTATACCGCTTATGATTAAGA	2520
Qy	1381	TTTAAATTTACGTTGGTGAAGAGTGAATTTTCTACCTTCAAAATAGCTTTTACGTTAT	1440	2461	TATTTATATCAGAAAAATAGATGAGTCCGAATTTAAAGCTTATACCGCTTATGATTAAGA	2520
Db	1381	TTTAAATTTACGTTGGTGAAGAGTGAATTTTCTACCTTCAAAATAGCTTTTACGTTAT	1440	2521	GGGTATATCGAAGATAGTCAAGATTTAGAAATCTATTTGATGCGCTTATGCGCTCAATTC	2580
Qy	1441	GCAGGAGAGGTAACGTTGATCTTTTAACTGAATTTTAACTGAGGATTAATAGTGTGCA	1500	2521	GGGTATATCGAAGATAGTCAAGATTTAGAAATCTATTTGATGCGCTTATGCGCTCAATTC	2580
Db	1441	GCAGGAGAGGTAACGTTGATCTTTTAACTGAATTTTAACTGAGGATTAATAGTGTGCA	1500	2581	GAATATAGTAAATGTCGAGGACCGGTTCTTTATGCGCTTTCCTTTAGCCCAAGTCCAAATC	2640
Qy	1501	CCTCGGAGAGGATATAGTCAATCGTTTATGCTATGCACTTTTGTTCAGGATCTGGAACA	1560	2581	GAATATAGTAAATGTCGAGGACCGGTTCTTTATGCGCTTTCCTTTAGCCCAAGTCCAAATC	2640
Db	1501	CCTCGGAGAGGATATAGTCAATCGTTTATGCTATGCACTTTTGTTCAGGATCTGGAACA	1560			

QY 2641 GGAAAGTGTGGAGACCGAATCGATCGCGCCACACCTTGAATGGATCTGTATAGAT 2700
DB 2641 GGAAAGTGTGGAGACCGAATCGATCGCGCCACACCTTGAATGGATCTGTATAGAT 2700
QY 2701 TGTTCCTGCAG 2711
DB 2701 TGTTCCTGCAG 2711

RESULT 3

US-08-465-609-4
; Sequence 4, Application US/08465609
; Patent No. 5866784
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: PREVENTION OF Bt RESISTANCE DEVELOPMENT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: The George Mason Building, Washington &
; STREET: Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,609
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,274
; FILING DATE:
; APPLICATION NUMBER: US 07/640,400
; FILING DATE: 22-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: P36,113
; REFERENCE/DOCKET NUMBER: 010830-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; TELEX: 440580
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3923 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 234..3803
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..233
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 3804..3923
US-08-465-609-4

Query Match 98.3%; Score 2664; DB 2; Length 3923;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2679; Conservative 25; Indels 0; Gaps 0;
QY 8 AATAGAATCTCAATCTCGATGACTGCTTTAGTCTTTTAAATCTGTCTACTTGACAGGGG 67

DB 1 AATAGAATCTCAATCTCGATGACTGCTTTAGTCTTTTAAATCTGTCTACTTGACAGGGG 60
QY 68 TAGGAACATAAATCGGTCAATTTTAAATATGCGGCATATATGATATTTTATATAAATTTGT 127
DB 61 TAGGAACATAAATCGGTCAATTTTAAATATGCGGCATATATGATATTTTATATAAATTTGT 120
QY 128 TAGGTTTTTGTATTTTTCATAAAGATGTCTCATATGTAATAAATCGTGTAAATGAAAAA 187
DB 121 TAGGTTTTTGTATTTTTCATAAAGATGTCTCATATGTAATAAATCGTGTAAATGAAAAA 180
QY 188 CAGTATCAAACTATCAGAACCTTTTGTAGTTTAAATAAAAAAGGAGGTATTTTATCGAGG 247
DB 181 CAGTATCAAACTATCAGAACCTTTTGTAGTTTAAATAAAAAAGGAGGTATTTTATCGAGG 240
QY 248 AAAATAATCAAAATCAATCTACATCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTTT 307
DB 241 AAAATAATCAAAATCAATCTACATCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTTT 300
QY 308 TGGATGGAGAACGGATATCAACTGGTAAATTAATCAATTTGATATTTCTCTGTCACTTTGTTTC 367
DB 301 TGGATGGAGAACGGATATCAACTGGTAAATTTCAATCAATTTGATATTTCTCTGTCACTTTGTTTC 360
QY 368 AGTTTCTGTATCTAACTTTTGTACAGGGGAGGATTTTGTAGTTGGAATTAATAGATTTTG 427
DB 361 AGTTTCTGTATCTAACTTTTGTACAGGGGAGGATTTTGTAGTTGGAATTAATAGATTTTG 420
QY 428 TATGGGAATAGTTGCGCCCTTCTCAATGGGATGCAATTTCTAGTACAAAATGGAACAATTA 487
DB 421 TATGGGAATAGTTGCGCCCTTCTCAATGGGATGCAATTTCTAGTACAAAATGGAACAATTA 480
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DB 481 TTAATGAAAGATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAAATTTAGAGGATTA 540
QY 548 GAAACAATTTCAATATATATGTTGAAGCAATTTAAAGAATGGGAAGAGATCTTAATAATC 607
DB 541 GAAACAATTTCAATATATATGTTGAAGCAATTTAAAGAATGGGAAGAGATCTTAATAATC 600
QY 608 CAGCAACAGGACAGAGTAATTTGATCGCTTTCTGATATCTTCACTGGGCTACTTGAAGGG 667
DB 601 CAGCAACAGGACAGAGTAATTTGATCGCTTTCTGATATCTTCACTGGGCTACTTGAAGGG 660
QY 668 ACATTCCTTTCTGTTTCTGAAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAG 727
DB 661 ACATTCCTTTCTGTTTCTGAAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTATGCTCAAG 720
QY 728 CGGCCAATCTGCATCTAGCTATATTAAGAGATCTGTAATTTTGTGGAGAAAGATTTGGGAT 787
DB 721 CGGCCAATCTGCATCTAGCTATATTAAGAGATCTGTAATTTTGTGGAGAAAGATTTGGGAT 780
QY 788 TGACAACGATAAATGCTCAATGAATACTATATAGACTAATAGGCATATTTGATGAATATG 847
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QY 848 CTGATCACTGTGCAAAATACGTATATCGGGATTTAAATAAATTTACCGAAATCTAGCTATC 907
DB 841 CTGATCACTGTGCAAAATACGTATATCGGGATTTAAATAAATTTACCGAAATCTAGCTATC 900
QY 908 AAGATTGGATAACATATATTAATCGATTACCGAGAGACTTAAACATTGCTGTATTTAGATATCG 967
DB 901 AAGATTGGATAACATATATTAATCGATTACCGAGAGACTTAAACATTGCTGTATTTAGATATCG 960
QY 968 CCGCTTTCTTTCCRAAATATGCAATAGGATATCCAAATTTAGCCAGCTTGGTCAACTAA 1027
DB 961 CCGCTTTCTTTCCRAAATATGCAATAGGATATCCAAATTTAGCCAGCTTGGTCAACTAA 1020
QY 1028 CAAGGAAGTTTATACGAGACCATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1087
DB 1021 CAAGGAAGTTTATACGAGACCATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1080
QY 1088 AATTAACCTCTTTTAAACGTTATGGAGAGCAGCGCAATTTAGAAATCTCTCATTTTATTTGATA 1147

Db	1081	AAATTAACCTCTTTAAAGTATGAGAGCAGCGCAATAGAAATCTCAATTTATTTGATA	1140
Qy	1148	TATTAATTAATCTTAAATCTTTACCGATGCTTTAGCTTTGAGCGCAATTTTATTTGG	1207
Db	1141	TATTAATTAATCTTAAATCTTTACCGATGCTTTAGCTTTGAGCGCAATTTTATTTGG	1200
Qy	1208	GAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTACATACATCTCTATATAG	1267
Db	1201	GAGGACATCGAGTAATATCTAGCTTTATAGGAGTGGTACATACATCTCTATATAG	1260
Qy	1268	GAAGAGAGGCGAACCAGGAGCTTCAAGATCTTTTACCTTTTATAGACCGGTATTTAG	1327
Db	1261	GAAGAGAGGCGAACCAGGAGCTTCAAGATCTTTTACCTTTTATAGACCGGTATTTAG	1320
Qy	1328	CTTTATCAATCTCTACTTTTACGATTTATACAGCACTTTCAGCGCCACCACTTTAAT	1387
Db	1321	CTTTATCAATCTCTACTTTTACGATTTATACAGCACTTTCAGCGCCACCACTTTAAT	1380
Qy	1388	TACGTGGTGGTGAAGGAGTGAATTTTCTACACCTTACCAATAGCTTTAGCTATGAGAA	1447
Db	1381	TACGTGGTGGTGAAGGAGTGAATTTTCTACACCTTACCAATAGCTTTAGCTATGAGAA	1440
Qy	1448	GAGGTACGCTTGAATCTTTAACTGAATTTACCGCTGAGGATAATAGTGTGCCACCTCGCG	1507
Db	1441	GAGGTACGCTTGAATCTTTAACTGAATTTACCGCTGAGGATAATAGTGTGCCACCTCGCG	1500
Qy	1508	AGGATATGCTCATCTTTATGTCATCACTTTTGTTCAAAGATCTGGAACACCTTTT	1567
Db	1501	AGGATATGCTCATCTTTATGTCATCACTTTTGTTCAAAGATCTGGAACACCTTTT	1560
Qy	1568	TAACAACTGGTGTAGTATTTCTTGGAGCGATGCTAGTCAACTTTTACCAATACAAATTTG	1627
Db	1561	TAACAACTGGTGTAGTATTTCTTGGAGCGATGCTAGTCAACTTTTACCAATACAAATTTG	1620
Qy	1628	ATCCAGAGAGATTAATCAATACCTTTAGTGAAGGATTTAGTGTGGGGGGCACT	1687
Db	1621	ATCCAGAGAGATTAATCAATACCTTTAGTGAAGGATTTAGTGTGGGGGGCACT	1680
Qy	1688	CTGTCAATTAAGGACAGGATTTACAGAGGGATATCTTGGAGGAATACCTTTGCTG	1747
Db	1681	CTGTCAATTAAGGACAGGATTTACAGAGGGATATCTTGGAGGAATACCTTTGCTG	1740
Qy	1748	ATTTGTATCTCTCAAGTCAATATTAATTCACCAATACCCCAAGTACCTTTAGAT	1807
Db	1741	ATTTGTATCTCTCAAGTCAATATTAATTCACCAATACCCCAAGTACCTTTAGAT	1800
Qy	1808	TTTGTAGCTTCCAGTACGAGTACGAGTATAGTATTAACAGGAGCGGATCCACAG	1867
Db	1801	TTTGTAGCTTCCAGTACGAGTACGAGTATAGTATTAACAGGAGCGGATCCACAG	1860
Qy	1868	GAGTGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAAGAACTATGAAATAGGGGGA	1927
Db	1861	GAGTGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAAGAACTATGAAATAGGGGGA	1920
Qy	1928	ACTTAACATCTAGAACATTTAGATATACCGATTTTATGATCTTTTCAATTTAGAGCTA	1987
Db	1921	ACTTAACATCTAGAACATTTAGATATACCGATTTTATGATCTTTTCAATTTAGAGCTA	1980
Qy	1988	ATCCAGATATATTTGGATTAAGTGAACACCTCTATTTGGTGCAGGTTCTATTTAGTAGC	2047
Db	1981	ATCCAGATATATTTGGATTAAGTGAACACCTCTATTTGGTGCAGGTTCTATTTAGTAGC	2040
Qy	2048	TTCAACTTTATATAGATAAAATTTGAATTTATTTAGCAGATGCAACATTTGAAGCAGAT	2107
Db	2041	TTCAACTTTATATAGATAAAATTTGAATTTATTTAGCAGATGCAACATTTGAAGCAGAT	2100
Qy	2108	CTGATTTAGAGAGCACAAGCGGTGAATGCGCTTTTACTTTCTTCCCAATCAATATG	2167
Db	2101	CTGATTTAGAGAGCACAAGCGGTGAATGCGCTTTTACTTTCTTCCCAATCAATATG	2160
Qy	2168	GGTTAAAAACCGATGTGACGATATCATTTGATCAAGTATCCCAATTTAGTGGATGTT	2227
Db	2161	GGTTAAAAACCGATGTGACGATATCATTTGATCAAGTATCCCAATTTAGTGGATGTT	2220

Qy	2228	TATCAGATGAATTTTGTCTGATGAAAGGCGAGAAATTTGTCGAGAAATCCAAACATCGCA	2287
Db	2221	TATCAGATGAATTTTGTCTGATGAAAGGCGAGAAATTTGTCGAGAAATCCAAACATCGCA	2280
Qy	2288	AGCGACTCAGTGTAGTACGCGGAAATTTTACCTTCAAGATCCAAACTTTAGAGGATCAATAGAC	2347
Db	2281	AGCGACTCAGTGTAGTACGCGGAAATTTTACCTTCAAGATCCAAACTTTAGAGGATCAATAGAC	2340
Qy	2348	AACCAAGCGTGGCTGGAGAGAGTACAGATATTTACCATCCAAAGGAGATGACGTAT	2407
Db	2341	AACCAAGCGTGGCTGGAGAGAGTACAGATATTTACCATCCAAAGGAGATGACGTAT	2400
Qy	2408	TCAAGAGAAATTTAGTCCACACTACCGGTACCGTTGATGAGTGTCTATCCAACTGATTTAT	2467
Db	2401	TCAAGAGAAATTTAGTCCACACTACCGGTACCGTTGATGAGTGTCTATCCAACTGATTTAT	2460
Qy	2468	ATCAGAAATAGTACGCTGAAATTAAGGCTTATACCGCTTATGAAATTAAGAGGGTATA	2527
Db	2461	ATCAGAAATAGTACGCTGAAATTAAGGCTTATACCGCTTATGAAATTAAGAGGGTATA	2520
Qy	2528	TCCAGATAGTCAAGCTTTAGAAATCTATTTGATCGGTACAAATGCAAAACACGAAATAG	2587
Db	2521	TCCAGATAGTCAAGCTTTAGAAATCTATTTGATCGGTACAAATGCAAAACACGAAATAG	2580
Qy	2588	TAAATGTCAGGACGCTTCTTATGCGCTTATGCGGTACAAATGCAAAACACGAAATAG	2647
Db	2581	TAAATGTCAGGACGCTTCTTATGCGCTTATGCGGTACAAATGCAAAACACGAAATAG	2640
Qy	2648	GTGAGAACCGGATCGATGCGGCGCACACCTTGAATGGAATCTGATCTAGATTTCTT	2707
Db	2641	GTGAGAACCGGATCGATGCGGCGCACACCTTGAATGGAATCTGATCTAGATTTCTT	2700
Qy	2708	GCAG 2711	
Db	2701	GCAG 2704	

RESULT 4
US-09-176-320-7
; Sequence 7, Application US/09176320
; Patent No. 6172281
; GENERAL INFORMATION:
; APPLICANT: Van Mellaert, Herman
; APPLICANT: Botterman, Johan
; APPLICANT: Van Rie, Jeroen
; APPLICANT: Joos, Henk
; TITLE OF INVENTION: PREVENTION OF BT RESISTANCE DEVELOPMENT
; FILE REFERENCE: 021565-052
; CURRENT APPLICATION NUMBER: US/09/176,320
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: PCT/EP90/00905
; EARLIER FILING DATE: 1990-05-30
; EARLIER APPLICATION NUMBER: GB 89401499.2
; EARLIER FILING DATE: 1989-05-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 3923
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (234)..(3803)
US-09-176-320-7
Query Match 98.1%; Score 2659.2; DB 3; Length 3923;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2676; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 128 TAGGTTTTTTGTATTTTTTTCATAAGATGTCTCATATGTATTAATCGTGTAAATGAATAA 187
DB 121 TAGGTTTTTTGTATTTTTTTCATAAGATGTCTCATATGTATTAATCGTGTAAATGAATAA 180
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DB 181 CAGTATCAAACTATCAGAACTTTTGGTAGTTTAAATAAAAAACGAGGTATTTTATGGAGG 240
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DB 1021 CAAGGGAAGTTTATACGGAACCAATTAATTAATTTTAAATCCACAGTTTACGTCTAGCTC 1080
QY 1088 AATTACTACTTTTAACTGATTTAGGAGCAGCGCAATTTAGAAATCTCTCAATTTATTTGATA 1147
DB 1081 AATTACTACTTTTAACTGATTTAGGAGCAGCGCAATTTAGAAATCTCTCAATTTATTTGATA 1140

QY 1148 TATTGAATAATCTTACAATCTTTTACGATTTGGTTTGTAGTTGGACGCAATTTTATATGGG 1207
DB 1141 TATTGAATAATCTTACAATCTTTTACGATTTGGTTTGTAGTTGGACGCAATTTTATATGGG 1200
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DB 1201 GAGGACATCGAGTATATCTAGCTTATAGGAGGTGTAAACATACATCTCTCTATATATG 1260
QY 1268 GAAGAGAGCGCAACAGGAGCCTCCAAGATCTCTTACTTTTAAATGGACCGGTATTTAGGA 1327
DB 1261 GAAGAGAGCGCAACAGGAGCCTCCAAGATCTCTTACTTTTAAATGGACCGGTATTTAGGA 1320
QY 1328 CTTTATCAATCTCTACTTTTACGATTTTACAGCAACCTTGGCCAGCGCCACCAATTTAAT 1387
DB 1321 CTTTATCAATCTCTACTTTTACGATTTTACAGCAACCTTGGCCAGCGCCACCAATTTAAT 1380
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DB 1381 TACGTGGTGTGAAGGAGTAGAATTTTCTACACCTCAAAATAGCTTTTACGTATCGAGGA 1440
QY 1448 GAGGTACCGTTTGAATTTTAACTGAATTTACCGCTGAGGATTAATAGTGTGCCACCTCGCG 1507
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DB 1501 AAGGATATAGTCAATCGTTTATGTCAATCAACTTTTGTCAAAGATCTCGAAACACCTTTT 1560
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DB 1801 TTCTGTTACGCTTTCAGTAGGAGTACAGAGTTTATAGTATTAACAGAGCGGATCCACAG 1860
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QY 1928 ACTTAAATCTAGAACATTTAGATATACCGATTTTGTAGTAACTTTTCAATTTAGAGCTA 1987
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QY 1988 ATCCAGATATATTTGGGATAAGTGAACCAACCTCTATTTTGTGTGCGAGTTCTTATAGTCG 2047
DB 1981 ATCCAGATATATTTGGGATAAGTGAACCAACCTCTATTTTGTGTGCGAGTTCTTATAGTCG 2040
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QY 2228 TATCAGATGAATTTTGTCTCGATGAAAGAGCGAGAAATTTGTCGAGAGAAAGTCAAAACATGCGA 2287

us-09-918-485-1.rni

Wed Oct 15 11:56:11 2003

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2281	DB	AGCGACTCAGTGTGATGAGCGGAATTTTACTTTCAAGATCCAAACTTCAGAGGGATCAATAGAC	2340
2348	DY	AACCCAGACCGTGGCTGCGAGAGGAAGTACACAGATATTACCATCCAAAGGAGGAGTACGCTAT	2407
2341	DB	AACCCAGACCGTGGCTGCGAGAGGAAGTACACAGATATTACCATCCAAAGGAGGAGTACGCTAT	2400
2408	DY	TCAAAGNGAATTAGCTCACACTACCGGGTACCGTGTGATGAGTGCTATCCAAAGCTATTAT	2467
2401	DB	TCAAAGNGAATTAGCTCACACTACCGGGTACCGTGTGATGAGTGCTATCCAAAGCTATTAT	2460
2468	DY	ATCAGAAATAGATAGCTGCAGAAATTTAAAGCTTATACCCGTTATGAATTAAGAGGGTATA	2527
2461	DB	ATCAGAAATAGATAGCTGCAGAAATTTAAAGCTTATACCCGTTATGAATTAAGAGGGTATA	2520
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2588	DY	TAAATGTGCAGGCGACGGGTTCTTATATGGCGCTTTACGCCCAAGTCCAAATCGCAAGT	2647
2581	DB	TAAATGTGCAGGCGACGGGTTCTTATATGGCGCTTTACGCCCAAGTCCAAATCGCAAGT	2640
2648	DY	GTGGAGAACCGAATCGATGCGCGCCACACCTTTGAATGGAAATCCTGATCTAGATCTGCTCT	2707
2641	DB	GTGGAGAACCGAATCGATGCGCGCCACACCTTTGAATGGAAATCCTGATCTAGATCTGCTCT	2700
2708	DY	GCAG 2711	
2701	DB	GCAG 2704	

RESULT 5

US-08-602-737-1

US-08-002-737-1
; Sequence 1, Application US/08602737

Patent No. 5736131

; PACIFIC NO. 3750151
; GENERAL INFORMATION:

APPLICANT: Bosch, Hendrick J

APPLICANT: Stiekema, Willem J

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: SANDOZ AGRO. INC

STREET: 975 California Avenue

;
SIRE: Palo Alto
;
CITY: Palo Alto
;

STATE: California

COUNTRY: USA

COUNTRY: USA
ZIP: CA 94304

;; ZLF: CH 54304
;; COMPUTER READABLE FORM:

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;; COMPUTER READABLE FORM.  
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible

COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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;
; SOFTWARE: FACEWIN RE
;
; CURRENT APPLICATION DATA:
;

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;;
CURRENT AFFILIATION DATA:
;;
APPLICATION NUMBER: US/08/602,737
;;

APPLICATION NUMBER: US/08/96-000000
FILING DATE: 21-FEB-1996

FILING DATE: 21-FEB-1990
CLASSIFICATION: 514

CLASSIFICATION: 314
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENCY INFORMATION:
NAME: Marcus-Wyner, Lynn

NAME: MARCUS-WYMER, DYM
REGISTRATION NUMBER: 34,869

REGISTRATION NUMBER: 34,800
REFERENCE/DOCKET NUMBER: 130-4080

; REFERENCE/DOCID NUMBER: 130
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-354-3588

TELEPHONE: 415-334-3500
TELEFAX: 415-857-1125

; ;
; TELEFAX: 413-837-1123
; INFORMATION FOR SEQ ID NO: 1:

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; INFORMATION FOR SEQ ID NO: 1
;
; SEQUENCE CHARACTERISTICS:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs

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; LENGTH: 3507 base pairs
; TYPE: nucleic acid
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TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: unknown
MOLSCULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567
US-08-602-737-1

Query Match 89.7%; Score 2431; DB 1; Length 3567;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2446; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

[illegible]

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1321 TTTAGGACTTTTCAATCTCTTCACTTTTACGATTTATACAGCAACTTGGCCAGCGCACCA 1380
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1681 GGCACCTCTGTCAATACAGGACAGGATTTACAGGAGGGGATATCTTCGAAAGAAATACC 1740
1441 GGCACCTCTGTCAATACAGGACAGGATTTACAGGAGGGGATATCTTCGAAAGAAATACC 1500
1741 TTTGGTGAATTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCAAGATACCGT 1800
1501 TTTGGTGAATTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCAAGATACCGT 1560
1801 TTAAGATTTTGTAGCTTCCAGTGGGATGAGGATGAGTATAGTATTAACAGAGCGGCA 1860
1561 TTAAGATTTTGTAGCTTCCAGTGGGATGAGGATGAGTATAGTATTAACAGAGCGGCA 1620
1861 TCCACAGGAGTGGGAGCGGCAAGTTAGTGTAGATATGCTCTTTCAGAAACTATGGAATA 1920
1621 TCCACAGGAGTGGGAGCGGCAAGTTAGTGTAGATATGCTCTTTCAGAAACTATGGAATA 1680
1921 GGGGAGAACTTAACTATAGAACATTTAGATATACGATTTTGTAGTAACTCTTTTCAATTT 1980
1681 GGGGAGAACTTAACTATAGAACATTTAGATATACGATTTTGTAGTAACTCTTTTCAATTT 1740
1981 AGAGCTAATCCAGATATATTTGGATAGTGAACCTCTTATTTGGTGACGTTCTATT 2040
1741 AGAGCTAATCCAGATATATTTGGATAGTGAACCTCTTATTTGGTGACGTTCTATT 1800
2041 AGTAGCGTTGAATCTTATATAGATAAAATTTGAAATTTTCTAGCAGATGCAACATTTGAA 2100
1801 AGTAGCGTTGAATCTTATATAGATAAAATTTGAAATTTTCTAGCAGATGCAACATTTGAA 1860
2101 GCAGAACTTGAATTTGAAAGAGACAAAAGCGGTTGAATGCGCTGTTTCTTTCCAAAT 2160
1861 GCAGAACTTGAATTTGAAAGAGACAAAAGCGGTTGAATGCGCTGTTTCTTTCCAAAT 1920
2161 CAAATCGGTTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAATTTAGTG 2220
1921 CAAATCGGTTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAATTTAGTG 1980

2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAAGCGAGAAATTTCTCGAGAAAGTCAAA 2280
1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAAAGCGAGAAATTTCTCGAGAAAGTCAAA 2040
2281 CATGGAAGCGACTCAGTGTATGAGCGGAATTTTACTTCAAGATCCAAACTTTCAGAGGGATC 2340
2041 CATGGAAGCGACTCAGTGTATGAGCGGAATTTTACTTCAAGATCCAAACTTTCAGAGGGATC 2100
2341 AATAGACAACACAGACCGCTGGCTGGAGAGGAAGTACAGATATTTACCATCCAGAGGAGAT 2400
2101 AATAGACAACACAGACCGCTGGCTGGAGAGGAAGTACAGATATTTACCATCCAGAGGAGAT 2160
2401 GACGTTATTCAAAGAGAAATTTACGTCACACTACCGGTTACCGTTTGTAGTGCCTATCCAAAG 2460
2161 GACGTTATTCAAAGAGAAATTTACGTCACACTACCGGTTACCGTTTGTAGTGCCTATCCAAAG 2220
2461 TATTATATCAGAAAAATAGATGAGTGCAGAAATTTAAAAAGCTTATACCGTTTATGAATTAAGA 2520
2221 TATTATATCAGAAAAATAGATGAGTGCAGAAATTTAAAAAGCTTATACCGTTTATGAATTAAGA 2280
2521 GGGTATATCGAAGATAGTCAAGACTTACAGACTTACAGAAATCTTATTTGATCGCTGCAAAACAC 2580
2281 GGGTATATCGAAGATAGTCAAGACTTACAGACTTACAGAAATCTTATTTGATCGCTGCAAAACAC 2340
2581 GAAATAGTAAATGTGCCAGGCAACGGGTTCTTTATGCGCGCTTTTCAGCCCAAAAGTCCAATC 2640
2341 GAAATAGTAAATGTGCCAGGCAACGGGTTCTTTATGCGCGCTTTTCAGCCCAAAAGTCCAATC 2400
2641 GGAAGTGTGAGAAACCGAATCGATGCGGCGCACACTTGAATGAATCCTGATCTAGAT 2700
2401 GGAAGTGTGAGAAACCGAATCGATGCGGCGCACACTTGAATGAATCCTGATCTAGAT 2460
2701 TGTTCTCTGACG 2711
2461 TGTTCTCTGACG 2471

RESULT 6

US-09-001-982-1
; Sequence 1, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Stiekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001.982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689

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/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 3567 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: unknown
/   MOLECULE TYPE: cDNA
/   HYPOTHETICAL: NO
/   ANTI-SENSE: NO
/   ORIGINAL SOURCE:
/     ORGANISM: Bacillus thuringiensis
/     FEATURE:
/       NAME/KEY: CDS
/       LOCATION: 1..3567
/
/ US-09-001-982-1
/
/ Query Match      89.7%; Score 2431; DB 3; Length 3567;
/ Best Local Similarity 99.0%; Pred. No. 0;
/ Matches 2446; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
/
/ QY      241  ATCGAGGAAAAATAATCAAAATCAATGCATACCTTACAAATGTGTTAACTAAATCTGAGAA 300
/ DB      1   ATCGAGGAAAAATAATCAAAATCAATGCATACCTTACAAATGTGTTAACTAAATCTGAGAA 60
/
/ QY      301  GTACTTTTGGATGAGAACGATCAACTCGTAAATTAATCAATTTGATATTTCTCTGTCA 360
/ DB      61  GTACTTTTGGATGAGAACGATCAACTCGTAAATTAATCAATTTGATATTTCTCTGTCA 120
/
/ QY      361  CTTGTTCAAGTCTTGCTATCTACTTTCGACAGGGGAGGATTTTGTAGTTGGATTAATA 420
/ DB      121  CTTGTTCAAGTCTTGCTATCTACTTTCGACAGGGGAGGATTTTGTAGTTGGATTAATA 180
/
/ QY      421  GATTTTGTATGGGNAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTGAA 480
/ DB      181  GATTTTGTATGGGNAATAGTTGGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTGAA 240
/
/ QY      481  CAATTAATTAATGAAAGAAATAGCTGAAATTTCTGTAGGAAGTCTGCTATTTGCTAAATTTAGAA 540
/ DB      241  CAATTAATTAATGAAAGAAATAGCTGAAATTTCTGTAGGAAGTCTGCTATTTGCTAAATTTAGAA 300
/
/ QY      541  GGATTAGGAAAACAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAGAGATCCT 600
/ DB      301  GGATTAGGAAAACAATTTCAATATATATGTGGAGCAATTTAAAGATGGGAGAGATCCT 360
/
/ QY      601  AATAATCCAGAACACAGGACAGAGTAATATGATCGCTTTCGTAATCTGATCGGCTACTT 660
/ DB      361  AATAATCCAGAACACAGGACAGAGTAATATGATCGCTTTCGTAATCTGATCGGCTACTT 420
/
/ QY      661  GAAAGGACAAATCTCTTCGTTTTCGAAATTTCTGAAATTTGAAATGACCCCTTTATTCGGTTAT 720
/ DB      421  GAAAGGACAAATCTCTTCGTTTTCGAAATTTCTGAAATTTGAAATGACCCCTTTATTCGGTTAT 480
/
/ QY      721  GCTCAAGCGGCCAATCTGCATCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
/ DB      481  GCTCAAGCGGCCAATCTGCATCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
/
/ QY      781  TTGGGATTTGACACGATAAATGTCATGAAACTATAATAGACTTAATAGGCATATTGAT 840
/ DB      541  TTGGGATTTGACACGATAAATGTCATGAAACTATAATAGACTTAATAGGCATATTGAT 600
/
/ QY      841  GAATATGCTGATCAGTGTGCAAAATACGTAATAATCGGGCAATTAATAATTTATCCGAAATCT 900
/ DB      601  GAATATGCTGATCAGTGTGCAAAATACGTAATAATCGGGCAATTAATAATTTATCCGAAATCT 660
/
/ QY      901  ACGTATCAAGATTGGATATACATATATTCGATTACGGAGAGACTTAACATTGACTGTATTA 960
/ DB      661  ACGTATCAAGATTGGATATACATATATTCGATTACGGAGAGACTTAACATTGACTGTATTA 720
/
/ QY      961  GATATCGCGGCTTCTTTTCAAACTATGACATAGAGGATATCCAATTCAGCCAGTGGT 1020
/ DB      721  GATATCGCGGCTTCTTTTCAAACTATGACATAGAGGATATCCAATTCAGCCAGTGGT 780
/
/ QY      1021  CAACTAAACAAGGGAAAGTTTATACGGACCCATTAATTAATTTTATCCACAGTTACAGTCT 1080

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200

Db	781	CAAC	TAA	CAGGGAAGT	TTATAC	GACCCATTAATTAATTTAATCCACAGTTACAGTCT	840	
Qy	1081	GTAGCT	CAAT	TACCTACT	TTTAAC	GTGTATGGAGACAGCGCAATTAGAATCCCTCATTTA	1140	
Db	841	GTAGCT	CAAT	TACCTACT	TTTAAC	GTGTATGGAGACAGCGCAATTAGAATCCCTCATTTA	900	
Qy	1141	TTTGAT	TATATTGAAT	AATCTTAA	CAATCTTTA	CGGAATGGTTTAGTTGTGGAGCGCAATTTT	1200	
Db	901	TTTGAT	TATATTGAAT	AATCTTAA	CAATCTTTA	CGGAATGGTTTAGTTGTGGAGCGCAATTTT	960	
Qy	1201	TATTTGGG	GAGCACA	TGAGTAAT	ACTAG	CTCTTATAGGAGGTGGTAACAATACTCTCT	1260	
Db	961	TATTTGGG	GAGCACA	TGAGTAAT	ACTAG	CTCTTATAGGAGGTGGTAACAATACTCTCT	1020	
Qy	1261	ATATATGG	AGAGGCGG	ACACAGAG	CGCTCAA	AGATCTCTTTATCTTTAATGGACCGGTA	1320	
Db	1021	ATATATGG	AGAGGCGG	ACACAGAG	CGCTCAA	AGATCTCTTTATCTTTAATGGACCGGTA	1080	
Qy	1321	TTTAGA	CTTTATCA	ATTCCTACT	TTTACGTAATTAAC	GACCACTCTGCCAGCGCCACCAT	1380	
Db	1081	TTTAGA	CTTTATCA	ATTCCTACT	TTTACGTAATTAAC	GACCACTCTGCCAGCGCCACCA	1140	
Qy	1381	TTTAA	TTTACG	FGTGTGA	AGAGT	AGATTTCTACACTCAACAATACCTTTACGTAT	1440	
Db	1141	TTTAA	TTTACG	FGTGTGA	AGAGT	AGATTTCTACACTCAACAATACCTTTACGTAT	1200	
Qy	1441	CGACG	AGAGGTAC	GGTTGATCTTTAA	CTGAACTAC	CGCTTAGGATTAATAGTGTGCCA	1500	
Db	1201	CGACG	AGAGGTAC	GGTTGATCTTTAA	CTGAACTAC	CGCTTAGGATTAATAGTGTGCCA	1260	
Qy	1501	CCTCG	GAGGATATAG	TATCATCTTTATGT	CATGCAACTTTTGT	TCAAAGATCTGGMACA	1560	
Db	1261	CCTCG	GAGGATATAG	TATCATCTTTATGT	CATGCAACTTTTGT	TCAAAGATCTGGMACA	1320	
Qy	1561	CTTTT	TTTAA	CAACTGGTGTAGTATTTTCT	TTGGACGATCGTAGTGC	CAACTCTTACAAT	1620	
Db	1321	CTTTT	TTTAA	CAACTGGTGTAGTATTTTCT	TTGGACGATCGTAGTGC	CAACTCTTACAAT	1380	
Qy	1621	ACAA	TGATCCG	AGAGAAATTAATCA	AATACCTTTAGTGA	AAAGATTTAGAGTTTGGGG	1680	
Db	1381	ACAA	TGATCCG	AGAGAAATTAATCA	AATACCTTTAGTGA	AAAGATTTAGAGTTTGGGG	1440	
Qy	1681	GGC	ACCTCTGT	CATTTAC	GAGCAGGATTTAC	NGAGGCGATATCCTT	CGAAGAAATATCC	1740
Db	1441	GGC	ACCTCTGT	CATTTAC	GAGCAGGATTTAC	NGAGGCGATATCCTT	CGAAGAAATATCC	1500
Qy	1741	TTTGT	GAATTTGT	ATCTCTCA	AGTCANATTAATTA	ATTCACCAATTTAC	CAAGATACCGT	1800
Db	1501	TTTGT	GAATTTGT	ATCTCTCA	AGTCANATTAATTA	ATTCACCAATTTAC	CAAGATACCGT	1560
Qy	1801	TTA	AGATTTGGT	TATACGCTTCC	AGTAGG	ATGCAAGTATTAATTAAC	AGAGCGGCA	1860
Db	1561	TTA	AGATTTGGT	TATACGCTTCC	AGTAGG	ATGCAAGTATTAATTAAC	AGAGCGGCA	1620
Qy	1861	TCC	CAGCAGGTGG	GAGGCCAA	GTGTAGTATG	CTCTTTCAG	AAAACCTATGGAANTA	1920
Db	1621	TCC	CAGCAGGTGG	GAGGCCAA	GTGTAGTATG	CTCTTTCAG	AAAACCTATGGAANTA	1680
Qy	1921	GGG	GAGAACTTAA	CATCTAG	ACAATTTAG	ATATACCGATTTT	TAGTAATCCTTTTCAITTT	1980
Db	1681	GGG	GAGAACTTAA	CATCTAG	ACAATTTAG	ATATACCGATTTT	TAGTAATCCTTTTCAITTT	1740
Qy	1981	AG	AGCTTATCC	GAGATATAATTC	GGGTAAGTGA	ACAACCTCTTATTT	TGTGCAGAGTTCTATT	2040
Db	1741	AG	AGCTTATCC	GAGATATAATTC	GGGTAAGTGA	ACAACCTCTTATTT	TGTGCAGAGTTCTATT	1800
Qy	2041	AG	TAGCGTTGA	ACTTTATATAG	ATAAATTTGA	ATTTTCTTAG	CAGATGCAACATTTGAA	2100
Db	1801	AG	TAGCGTTGA	ACTTTATATAG	ATAAATTTGA	ATTTTCTTAG	CAGATGCAACATTTGAA	1860
Qy	2101	GC	AAATCTG	ATTTAG	AAAGACGACAA	AGGCGGTGA	ATGCCCTGTTTACTTCTTCCAAAT	2160


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Db 1861 GCAGAACTCTGATTAGAAAGACACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAT 1920
Qy 2161 CAAATCGGGTAAAAACCGATGTGACGGATATATATATGATCAAGTATCCATTTAGTG 2220
Db 1921 CAAATCGGGTAAAAACCGATGTGACGGATATATATATGATCAAGTATCCATTTAGTG 1980
Qy 2221 GATTGTTTATCAGATGAATTTTCTGATGAAAGCGGAAATGTCGGAAGATCAAA 2280
Db 1981 GATTGTTTATCAGATGAATTTTCTGATGAAAGCGGAAATGTCGGAAGATCAAA 2040
Qy 2281 CATGCGAAGCGACTCAGTGTATGATGCGAAATTTACTTCAAGATCAAACTTTCAGAGGATC 2340
Db 2041 CATGCGAAGCGACTCAGTGTATGATGCGAAATTTACTTCAAGATCAAACTTTCAGAGGATC 2100
Qy 2341 AATAGACAACCGACCGTGGCTGGAGGAGGATACAGATATTAACCATCCAGGAGGAT 2400
Db 2101 AATAGACAACCGACCGTGGCTGGAGGAGGATACAGATATTAACCATCCAGGAGGAT 2160
Qy 2401 GAGTATTCAAGAGAAATACGTACACTACCGGTACCGTGTGATGAGTGCTATCCAAG 2460
Db 2161 GAGTATTCAAGAGAAATACGTACACTACCGGTACCGTGTGATGAGTGCTATCCAAG 2220
Qy 2461 TATTATATCAGAAATAGATGATGCGAAATTAAGAGCTTATACCGTGTATGAATTAAG 2520
Db 2221 TATTATATCAGAAATAGATGATGCGAAATTAAGAGCTTATACCGTGTATGAATTAAG 2280
Qy 2521 GGTATATCAAGATAGTCAAGACTTAGAAATCTATTGATCGCGTACAAATGCAAAACAC 2580
Db 2281 GGTATATCAAGATAGTCAAGACTTAGAAATCTATTGATCGCGTACAAATGCAAAACAC 2340
Qy 2581 GAAATAGTAAATGTCGAGCAGCGGTTCCTTATGCGCGTTTCAGCCCAAAAGTCCAATC 2640
Db 2341 GAAATAGTAAATGTCGAGCAGCGGTTCCTTATGCGCGTTTCAGCCCAAAAGTCCAATC 2400
Qy 2641 GGAAGTGTGGAACCGGAATCGATCGCGCACACCTTGAATGGAATCCTGATCTAGAT 2700
Db 2401 GGAAGTGTGGAACCGGAATCGATCGCGCACACCTTGAATGGAATCCTGATCTAGAT 2460
Qy 2701 TGTCTCTGCAG 2711
Db 2461 TGTCTCTGCAG 2471

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RESULT 7

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US-07-828-788A-15
; Sequence 15, Application US/07828788A
; Patent No. 5273746
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/828,788A
; FILING DATE: 19920129
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75

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TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B2
; US-07-828-788A-15

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Query Match 89.6%; Score 2429.4; DB 1; Length 3567;

Best Local Similarity 98.9%; Pred. No. 0; Mismatches 26; Indels 0; Gaps 0;

Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 241 ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCGAAGAA 300
Db 1 ATGGAGGAAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCGAAGAA 60
Qy 301 GTACTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATGTATATTTCTGTGCA 360
Db 61 GTACTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATGTATATTTCTGTGCA 120
Qy 361 CTGTGTTGAGTTTCTGATATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTCGATTAATA 420
Db 121 CTGTGTTGAGTTTCTGATATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTCGATTAATA 180
Qy 421 GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 480
Db 181 GATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATTTGAA 240
Qy 481 CAATTAATTAATGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540
Db 241 CAATTAATTAATGAAAGAAATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 300
Qy 541 GGATTAGGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCT 600
Db 301 GGATTAGGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCT 360
Qy 601 AATAATCCAGCAACCGACGACAGATTAATGATCGCTTTTCGTATATCTTGTAGCGGTACTT 660
Db 361 AATAATCCAGCAACCGACGACAGATTAATGATCGCTTTTCGTATATCTTGTAGCGGTACTT 420
Qy 661 GAAAGGGAATTTCTGTTTGGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 720
Db 421 GAAAGGGAATTTCTGTTTGGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
Qy 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGA 780
Db 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTTCGAGAAAGA 540
Qy 781 TTGGGATTTGACAAACGATAAATGTCATGAAACTATAATAGACTAATTTAGGCATATTTGAT 840
Db 541 TTGGGATTTGACAAACGATAAATGTCATGAAACTATAATAGACTAATTTAGGCATATTTGAT 600
Qy 841 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATTTACCGAAATCT 900
Db 601 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATTTACCGAAATCT 660
Qy 901 ACGTATCAAGATTGGATAACATATTAATCGATTACCGAGAGACTTAACTTGAATCTATTA 960
Db 661 ACGTATCAAGATTGGATAACATATTAATCGATTACCGAGAGACTTAACTTGAATCTATTA 720

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QY	961	GATATCGCGCTTCTTTCCAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTGTGT	1020
Db	721	GATATCGCGCTTCTTTCCAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTGTGT	780
QY	1021	CACTAACAGGGAAGTTTATACGACCCATTAATTAATTTAAATCCACAGTACAGTCT	1080
Db	781	CACTAACAGGGAAGTTTATACGACCCATTAATTAATTTAAATCCACAGTACAGTCT	840
QY	1081	GTAGCTCAATTAACCTTTTAAAGTTATGAGAGAGAGCGCAATAGAAATCTCAATTTA	1140
Db	841	GTAGCTCAATTAACCTTTTAAAGTTATGAGAGAGAGCGCAATAGAAATCTCAATTTA	900
QY	1141	TTTGATATATGAAATATCAATCTTACAACTTTACGAGTTGTTAGTGTGGAGCGCAATTT	1200
Db	901	TTTGATATATGAAATATCAATCTTACAACTTTACGAGTTGTTAGTGTGGAGCGCAATTT	960
QY	1201	TATGGGGAGGACATCGAGTAATATCTAGCTTTATAGAGGTGTAACATAATCTCTCT	1260
Db	961	TATGGGGAGGACATCGAGTAATATCTAGCTTTATAGAGGTGTAACATAATCTCTCT	1020
QY	1261	ATATATGGAAGAGAGCGCAACAGGAGCTCCAGATCTCTTCTTTTAAATGGACCGGTA	1320
Db	1021	ATATATGGAAGAGAGCGCAACAGGAGCTCCAGATCTCTTCTTTTAAATGGACCGGTA	1080
QY	1321	TTTAGGACTTTATCAATCTCTTACAGTTTATACAGAACTCTGCGAGCGCACCAT	1380
Db	1081	TTTAGGACTTTATCAATCTCTTACAGTTTATACAGAACTCTGCGAGCGCACCAT	1140
QY	1381	TTTAAATTTAGCTGGTGGTGAAGGAGTAGAATTTTCAACCTCAATAGCTTTAGCTAT	1440
Db	1141	TTTAAATTTAGCTGGTGGTGAAGGAGTAGAATTTTCAACCTCAATAGCTTTAGCTAT	1200
QY	1441	GCAGAGAGAGTACGGTTCATTTCTTAACTGAAATACCGCTGAGGAGTAATAGTGTGCA	1500
Db	1201	CGAGAGAGAGTACGGTTCATTTCTTAACTGAAATACCGCTGAGGAGTAATAGTGTGCA	1260
QY	1501	CTCCGGAAGGATATAGTCAATCTTTATGTCATGCAACTTTTGTTCAGAGCTGGAACA	1560
Db	1261	CTCCGGAAGGATATAGTCAATCTTTATGTCATGCAACTTTTGTTCAGAGCTGGAACA	1320
QY	1561	CTTTTAACTCAACTGGTGTAGTATTTCTTGGACGCACTCGTAGTCAACTCTTCAAAAT	1620
Db	1321	CTTTTAACTCAACTGGTGTAGTATTTCTTGGACGCACTCGTAGTCAACTCTTCAAAAT	1380
QY	1621	ACAAATGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTAGAGTTGGGG	1680
Db	1381	ACAAATGATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGAGATTTAGAGTTGGGG	1440
QY	1681	GGCACTCTGTCNTACAGGACCGAGATTTACAGGAGGGGATATCTTCCGAAGAAATACC	1740
Db	1441	GGCACTCTGTCNTACAGGACCGAGATTTACAGGAGGGGATATCTTCCGAAGAAATACC	1500
QY	1741	TTTGGTGAATTTGTTATCTTACAGTCAATTAATTCACCAATTAACCAAGATACCGT	1800
Db	1501	TTTGGTGAATTTGTTATCTTACAGTCAATTAATTCACCAATTAACCAAGATACCGT	1560
QY	1801	TTAAGATTTGGTTCAGTTCAGTACGAGTCCAGGATATAGTATTAACAGGAGCGGCA	1860
Db	1561	TTAAGATTTGGTTCAGTTCAGTACGAGTCCAGGATATAGTATTAACAGGAGCGGCA	1620
QY	1861	TCCAAGAGTGGGAGGCGCAAGTTAGTATGATATGCTCTTCCAGAACTATGGAATA	1920
Db	1621	TCCAAGAGTGGGAGGCGCAAGTTAGTATGATATGCTCTTCCAGAACTATGGAATA	1680
QY	1921	GGGAGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTATCTTTTCAATTT	1980
Db	1681	GGGAGAGAACTTAACATCTAGAACATTTAGATATACCGATTTAGTATCTTTTCAATTT	1740
QY	1981	AGAGCTAATCCAGATATAATTTGGGATAGTGAACAACTCTTATTTGGTCCAGGTTCTATT	2040
Db	1741	AGAGCTAATCCAGATATAATTTGGGATAGTGAACAACTCTTATTTGGTCCAGGTTCTATT	1800
QY	2041	AGTACGCTTGAACTTTTATATAGATAAAATTTGAATTTATCTAGCAGATGCAACATTTGAA	2100

Db	1801	AGTAGCGGTGAACCTTTATATAGATAAAATTTGAATTTATCTAGCAGATGCAACATTTGAA	1860
QY	2101	GCAGAAATCTGATTTAGAAAGAGACAAAAGCGGTGAATGCCCTGTCTTCTTCTTCCAAAT	2160
Db	1861	GCAGAAATCTGATTTAGAAAGAGACAAAAGCGGTGAATGCCCTGTCTTCTTCTTCCAAAT	1920
QY	2161	CAATCCGGTTTAAACACCGATGTCACGATTTATCATATTTGATCAAGTATCCAAATTTAGTG	2220
Db	1921	CAATCCGGTTTAAACACCGATGTCACGATTTATCATATTTGATCAAGTATCCAAATTTAGTG	1980
QY	2221	GATTTCTTATCAGATCAATTTTGTCTGATGAAAGCGGAGAAATTTGTCGAGAAAGTCAAA	2280
Db	1981	GATTTCTTATCAGATCAATTTTGTCTGATGAAAGCGGAGAAATTTGTCGAGAAAGTCAAA	2040
QY	2281	CATGCGAGGAGCTCAGTCACTGAGCGGAATTTTACTTCAAGATCCAAACTTCAGAGGGATC	2340
Db	2041	CATGCGAGGAGCTCAGTCACTGAGCGGAATTTTACTTCAAGATCCAAACTTCAGAGGGATC	2100
QY	2341	ATAGACAAACGAGCGGTGGTGGAGGAGTACAGATATTACCATCCAAGGAGGAGAT	2400
Db	2101	ATAGACAAACGAGCGGTGGTGGAGGAGTACAGATATTACCATCCAAGGAGGAGAT	2160
QY	2401	GAGTATTTCAAAAGAGAAATTTAGCTCACTACCGGTACCGTGTGATGAGTGTATCCAAAG	2460
Db	2161	GAGTATTTCAAAAGAGAAATTTAGCTCACTACCGGTACCGTGTGATGAGTGTATCCAAAG	2220
QY	2461	TATTTATATCAGAAATATAGATGATGCGGAAATTTAAAGCTTTATACCGTTTGAATTAAGA	2520
Db	2221	TATTTATATCAGAAATATAGATGATGCGGAAATTTAAAGCTTTATACCGTTTGAATTAAGA	2280
QY	2521	GGGTATATCGAAGATAGTCAAGACTTTAGAAATCTATTGATGCGGTACATGGAACAC	2580
Db	2281	GGGTATATCGAAGATAGTCAAGACTTTAGAAATCTATTGATGCGGTACATGGAACAC	2340
QY	2581	GAAATAGTAAATGTCGACGACGCGGTCTCTTATGGCGCTTTTCAGCCCAAGTCCAAATC	2640
Db	2341	GAAATAGTAAATGTCGACGACGCGGTCTCTTATGGCGCTTTTCAGCCCAAGTCCAAATC	2400
QY	2641	GGAAAGTGTGAGAGAACCGAATCGATCGCGCCACACCTTGAATGGAATCTGATCTAGAT	2700
Db	2401	GGAAAGTGTGAGAGAACCGAATCGATCGCGCCACACCTTGAATGGAATCTGATCTAGAT	2460
QY	2701	TGTTCTCTGAG 2711	
Db	2461	TGTTCTCTGAG 2471	

RESULT 8
US-08-356-034-5
; Sequence 5, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; REGISTRATION NUMBER: 21,023
; REFERENCE/DOCKET NUMBER: MA43.C1.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B2
; US-08-356-034-5

Query Match 89.6%; Score 2429.4; DB 1; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATATCAAAATCAATGCATACCTTCAATTTGTTAAAGTAACTCTGAAGAA 300
DB 1 ATGGAGGAAATATCAAAATCAATGCATACCTTCAATTTGTTAAAGTAACTCTGAAGAA 60
QY 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCTCAATTTGATTTCTCTGTCA 360
DB 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCTCAATTTGATTTCTCTGTCA 120
QY 361 CTTGTTTCAGTTCTGTTATCTAATTTGTTACAGGGGGAGGATTTTGTAGTTGGAATTAATA 420
DB 121 CTTGTTTCAGTTCTGTTATCTAATTTGTTACAGGGGGAGGATTTTGTAGTTGGAATTAATA 180
QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGATGTCATTTCTAGTACAAATTTGAA 480
DB 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGATGTCATTTCTAGTACAAATTTGAA 240
QY 481 CAATTAATTAAGAAAGATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540
DB 241 CAATTAATTAAGAAAGATAGCTGAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 300
QY 541 GGATTTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAGAAATGGGAAGAGATCTCT 600
DB 301 GGATTTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAGAAATGGGAAGAGATCTCT 360
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DB 361 AATAATCCAGCAACAGGACAGAGTAAATTTGATCGCTTTGCTATCTGATGGCTACTTT 420
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421 GAAAGGGACATTCCTTCTGTTTGAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
721 GCTCAAGCGGCCAATCTGCTATCTAGCTATATTAAGAGATTCTGTTAATTTTGGAGAAAGA 780
481 GCTCAAGCGGCCAATCTGCTATCTAGCTATATTAAGAGATTCTGTTAATTTTGGAGAAAGA 540
781 TTGGGATTGACAAACGATAAATGTCAATGAAAACTATAATAGACTAATTAAGGCATATTGAT 840
541 TGGGGATTGACAAACGATAAATGTCAATGAAAACTATAATAGACTAATTAAGGCATATTGAT 600
841 GAATATGCTGATCACTGTGCAAAATAGCTAATCGGGGATTAATAATTTTACCGAAATCT 900
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1021 CAACTHAAAGGGAAGTTTATACGGACCCATTAATTTAATTTTAAATCCAGTTTACAGTCT 1080
781 CAACTHAAAGGGAAGTTTATACGGACCCATTAATTTAATTTTAAATCCAGTTTACAGTCT 840
1081 GTAGCTCAATTAACCTTTTAAACGTTATGGAGAGCGCAATTAAGAAATCTCAATTTA 1140
841 GTAGCTCAATTAACCTTTTAAACGTTATGGAGAGCGCAATTAAGAAATCTCAATTTA 900
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1081 TTTAGGACTTTTCAATCTTCTTACGATTTATACGAACTTTCAGCAACCTTGCAGCCACCA 1140
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1501 TTTGGTGAATTTTGTATCTCTCAAGTCAATTAATTAATTCACCAATTAACCAAGATACCGT 1560
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1561 TTAAGATTTTCGTAGCTTCCAGTAGGGATGAGAGTATTAATTAATTAACAGAGGCGCA 1620
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1621 TCCACAGAGTGGGAGGCGCAAGTTAGTGTAAATATGCTCTTCAGAAATCATGGAATA 1680
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1681 GGGGAGAACTTAAACATCTAGAAATTTAGATATACCGATTTTATGTAATCTTTTCATTT 1740
Db
1981 AGAGCTAATCCAGATATAATTTGGGATAGTGAACCACTCTTATTTGGTGGAGGTTCTATT 2040
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1741 AGAGCTAATCCAGATATAATTTGGGATAGTGAACCACTCTTATTTGGTGGAGGTTCTATT 1800
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2041 AGTAGCGTTGACCTTTATATAGATAAAATTTGAAATTTATCTAGCAGATCAACATTTGAA 2100
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1801 AGTAGCGTTGACCTTTATATAGATAAAATTTGAAATTTATCTAGCAGATCAACATTTGAA 1860
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2101 CGAATCTGATTTAGAAAGACCAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 2160
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1861 CGAATCTGATTTAGAAAGACCAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAAT 1920
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1981 GATTTGTTATCAGATCAATTTTGTCTGGATGAAGCGAATTTGTCGAGAAAGTCAAA 2040
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2281 CATGGAAGCGACTAGTGTGAGGAGTACAGATTTTACTTCAAGATCCAAATTTCAAGGGATC 2340
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2041 CATGGAAGCGACTAGTGTGAGGAGTACAGATTTTACTTCAAGATCCAAATTTCAAGGGATC 2100
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2101 AATAGCAACAGACCGTGTCTGGAGGAGTACAGATTTTACTTCAAGATCCAAATTTCAAGGGAT 2160
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2641 GGAAGTGTGGAGAACCGAATCGATCGCGCACACCTTGAATGGAATCTGTATCTAGAT 2700
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2401 GGAAGTGTGGAGAACCGAATCGATCGCGCACACCTTGAATGGAATCTGTATCTAGAT 2460
Db
2701 TGTTCCTGCAG 2711
Qy
2461 TGTTCCTGCAG 2471
Db

RESULT 9
US-08-980-071-1
; Sequence 1, Application US/08980071
; Patent No. 592118
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
4.

APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettius, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPTOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567
US-08-980-071-1

Query Match 89.6%; Score 2429.4; DB 2; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 241 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAATTTTAAAGTATCTCGAAGAA 300
Db 1 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAATTTTAAAGTATCTCGAAGAA 60
Qy 301 GTACTTTTGGATCGAGAGCGGATATCACTGGTAAATTAATCAATTTGATTTCTGTCA 360
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Qy 361 CTGTTCAGTTTCTGGTATCTAACTTTGTACCAAGGGGAGGATTTTGTGATTAATA 420
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DB 481 GCTCAAGCGGCCAATCTGCACTAGCTATATTAAGAGATCTCTAAATTTTTCGAGAAAGA 540
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DB 541 TTGGGATGCAACGATAAATGTCAATGAAACCTATAATAGACTAAATAGGCATATTGAT 600
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DB 661 ACCTATCAAGATTTGGATTAACATATAATCGATTTACGGAGAGACTTAACATTTGACTGTATTA 720
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DB 781 CAACCTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAACTCCACAGTTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTACTTTTAACTTTATGGAGAGAGCGCAATTAAGAAATCTCAATTA 1140
DB 841 GTAGCTCAATTAACCTACTTTTAACTTTATGGAGAGAGCGCAATTAAGAAATCTCAATTA 900
QY 1141 TTTGATATATTGAATTAATCTTACAACTCTTACCGATTTGGTTAGTTGTTGAGCCCAATTTT 1200
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QY 1201 TATTGGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGGTTTAAACATAATCTCTCT 1260
DB 961 TATTGGGGAGGACATCGAGTAATATCTAGCTTTATAGGAGGTTTAAACATAATCTCTCT 1020
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DB 1081 TTTAGGACTTTATCAATCTCTACTTTACGATTTATACAGCACTTTGCCAGCCACCAT 1140
QY 1381 TTTAAATTTACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTAT 1440
DB 1141 TTTAAATTTACGTGGTGGTGAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTAT 1200
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QY 1681 GGCACCTCTGTCTATTACAGACCCAGGATTTTACAGGAGGGGATATCTTCCGAGAAATACC 1740
DB 1441 GGCACCTCTGTCTATTACAGACCCAGGATTTTACAGGAGGGGATATCTTCCGAGAAATACC 1500

QY 1741 TTTGGTGATTTTGTATCTCTCAAGTCAATATAATTAATTCACCAATTAACCAAGATACCGT 1800
DB 1501 TTTGGTGATTTTGTATCTCTCAAGTCAATATAATTAATTCACCAATTAACCAAGATACCGT 1560
QY 1801 TTAAGATTTTGTACGCTTCCAGTAGGAGTGCAGAGTTATAGTATTAACAGGAGCGGCA 1860
DB 1561 TTAAGATTTTGTACGCTTCCAGTAGGAGTGCAGAGTTATAGTATTAACAGGAGCGGCA 1620
QY 1861 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTTCAGAAAACTATGGAATA 1920
DB 1621 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTTCAGAAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTATAGAACTATTAGATATACCGATTTTAGTAACTCTTTTCAAT 1980
DB 1681 GGGGAGAACTTAACTATAGAACTATTAGATATACCGATTTTAGTAACTCTTTTCAAT 1740
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DB 1741 AGAGCTTAATCCAGATATAATTTGGGATAAGTGAACAACCTCTATTTGGTGCAGGTTCTAT 1800
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DB 1801 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATCAACATTTGAA 1860
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DB 1861 GCAGAACTCTGATTTTAAAGAGACACAAAAGCGGTAATGCTCTTTACTTTCTTCCAAT 1920
QY 2161 CAATTCGGGTTAAACCCGATGTGAGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2220
DB 1921 CAATTCGGGTTAAACCCGATGTGAGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 1980
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DB 2041 CATCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGGATC 2100
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DB 2101 ATAGACAACAGACCGTGGCTGGAGAGGAGTACAGATATTTACCATCCAGGAGGAGAT 2160
QY 2401 GAGCTATTTCAGAGAAATTTACGTCACACTACCGGGTACCGTTGATGAGTGCTATCCAAAG 2460
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DB 2401 GGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTTGAATGGAATCTCTGATCTAGAT 2460
QY 2701 TGTTCTCTGAG 2711
DB 2461 TGTTCTCTGAG 2471

RESULT 10
US-08-980-071-11
; Sequence 11, Application US/08980071
; Patent No. 5914318

• Qy

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366	GAAGGGGACATTCCTTCGTTTCGAAATTCCTCGAATTTGAAGTACCCCTTTTATCCGTTTAT	720
421	GAAGGGGACATTCCTTCGTTTCGAAATTCCTCGAATTTGAAGTACCCCTTTTATCCGTTTAT	480
721	GCTCAAGCGGCGCATCTGCATCTAGCTATATTAAGAGATCTCTGTAATTTTGGAGAAAGA	780
481	GCTCAAGCGGCGCATCTGCATCTAGCTATATTAAGAGATCTCTGTAATTTTGGAGAAAGA	540
781	TTGGGATGTGAACAAGTAATGTCAATGAATAAAGTAAATATAGACTAAATTTAGGCGATATTGAT	840
541	TGGGGATGTGAACAAGTAATGTCAATGAATAAAGTAAATATAGACTAAATTTAGGCGATATTGAT	600
841	GAATATGCTGTGATCATCTGTGCAAAATACGTAATTAATCGGGGATTAATAATTTTACCGAAATCT	900
601	GAATATGCTGTGATCATCTGTGCAAAATACGTAATTAATCGGGGATTAATAATTTTACCGAAATCT	660
901	ACGTTATCAAGATTGGATAACATATAATTCGAAATTCGAGAGACTTTAAACATTCGTATTA	960
661	ACGTTATCAAGATTGGATAACATATAATTCGAAATTCGAGAGACTTTAAACATTCGTATTA	720
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1021	CAACTCAACGAGGAGAGTTTATACGAGCCCAATTAATTAATTTAAATCCACAGTTACAGTCT	1080
781	CAACTCAACGAGGAGAGTTTATACGAGCCCAATTAATTAATTTAAATCCACAGTTACAGTCT	840
1081	GTAGCTCAAAATACCTACTTTTAAAGCTTATGAGAGACGAGCAATAGAAATCCCTCATTTA	1140
841	GTAGCTCAAAATACCTACTTTTAAAGCTTATGAGAGACGAGCAATAGAAATCCCTCATTTA	900
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901	TTTGTATATATGGAATTAATCTTACAACTTTTACGATTTGGTTAGTCTGTGGACGCAATTTT	960
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961	TATTTGGGAGGACATCGAGTATATCTAGCCTTATAGGAGTGTGTAACATATAACATCTCTCT	1020
1261	ATATATGAGAGAGGCGGAACGAGGAGCTCCAGAGTCCCTTTACTTTTAAATGACCGGTA	1320
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1621	ACAATTTGATCCGAGAGGAATTAACAATAACCTTTAGTTCGAAAGGATTTTAGAGTTTGGGG	1680
1381	ACAATTTGATCCGAGAGGAATTAACAATAACCTTTAGTTCGAAAGGATTTTAGAGTTTGGGG	1440
1681	GGCACCTCTGTGCTATACAGGACCGAGGATTTTACAGGAGGGGATATCCTTTCGAGAAATATACC	1740

Db 1441 GGCACCTCTGTCATTACAGGACCGAGGATTTACAGGAGGGAGATCTCTCGAAGAAATACC 1500
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Db 1501 TTTGGTGATTTTGTATCTCTCAAGTCAATATTAATTCACCAATTAACCCAAAGATACCGT 1560
Qy 1801 TTAAGATTTGTTACGCTTCAGTAGGATGCGAGGTATATAGTATTAACAGAGCGGCA 1860
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Db 1861 GCAGAACTCTGAATTTAGAAAGAGACAAAAGCGGTGAATGCCCTGTTTACTTCTTCCAAT 1920
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Qy 2701 TGTTCTGCGAG 2711
Db 2461 TGTTCTGCGAG 2471

; Sequence 1, Application US/08757536
; Patent No. 5942664
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettub, Anne-Marie Light
; TITLE OF INVENTION: Bacillus thuringiensis CryIC
; TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
; NUMBER OF INVENTIONS: Making CryIC Mutants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White and Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,536
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3567 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3567
; US-08-757-536-1

Query Match 89.6%; Score 2429.4; DB 2; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db 1 ATGGAGGAAAATAATCAAAATCAATGCATACCTTCAATTTGTTTAAAGTAATCCTGAAGAA 60
Qy 301 GTACTTTTGGATGGAGAACGGATCAACTGTGTAAATTAATCAATTTGATTAATTTCTCTGTCA 360
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Qy 361 CTTGTTTCAGTTTCTGTTATCTAACTTTGTACAGGGGAGGATTTTGTAGTGGATTAATA 420
Db 121 CTTGTTTCAGTTTCTGTTATCTAACTTTGTACAGGGGAGGATTTTGTAGTGGATTAATA 180
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Db 301 GGATTTAGGAAACAATTTCAATATATATATGCGAGCATTTTAAGATGCGAAGATCCT 360
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1861 GCAGATCTGTATTTAGAAAGAGGACAAAGGCGGTGAATGCGCTGTTACTTCTTCCAAAT 1920
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1981 GATTTGTTATCAGATGAATTTCTCTGAGTGAAGGAGAGATTTGTCGAGAGAGTCAAA 2040
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2041 CATGCGAAGCGACTCAGTGTAGTGAAGGAGATTTCTCAAGATCCAAATCTTCAAGAGGATC 2100
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2101 AATAGACAACAGAGCGGTGGCTGGAGAGGAGTACAGATATTAATTAATTAATTAATTAATTAATTA 2160
2401 GACGTATTCAGAGAGATTTACGTCACTACCGGTTACCGTTGATGAGTGTCTATCCAAAG 2460
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2461 TATTTATATCAGAAATAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2520
2221 TATTTATATCAGAAATAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2280
2521 GGGTATATCGAAGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2580
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2581 GAATATGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2640
2341 GAATATGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2400
2641 GGAAGTGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
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2701 TGTCTCTGAG 2711
2461 TGTCTCTGAG 2471


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;; Sequence 11, Application US/08757536
;; Patent No. 5942664
;; GENERAL INFORMATION:
;; APPLICANT: Baun, James A.
;; APPLICANT: Gilmer, Amy Jelen
;; APPLICANT: Mettus, Anne-Marie Light
;; TITLE OF INVENTION: Bacillus thuringiensis CryIC
;; TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
;; TITLE OF INVENTION: Making CryIC Mutants
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White and Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: USA
;; ZIP: 77210-4433
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,536
;; FILING DATE: CONCURRENTLY HERewith
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kitchell, Barbara
;; REGISTRATION NUMBER: 33,928
;; REFERENCE/DOCKET NUMBER: MOBT:023
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3567 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..3567
;; US-08-757-536-11

Query Match      89.6%; Score 2429.4; DB 2; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY      241 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAAGAA 300
DB      1 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAAGAA 60

QY      301 GTACTTTTCGATGGAGACCGGATACCACTGGTAATTAATCAATGATATTTCTCTGTCA 360
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QY      361 CTGTGTCAGTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTGGATTAATA 420
DB      121 CTGTGTCAGTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTGGATTAATA 180

QY      421 GAATTTGTATGGGAATAGTGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
DB      181 GAATTTGTATGGGAATAGTGTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240

QY      481 CAATTAATTAAGGAAGATAGTGTGGCCCTTCTAGGAATGCTGCTATTTCTGCTAATTTAGAA 540
DB      241 CAATTAATTAAGGAAGATAGTGTGGCCCTTCTAGGAATGCTGCTATTTCTGCTAATTTAGAA 300

QY      541 GGAATAGGAAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGAAGAGATCCT 600
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QY      601 AATAATCCAGCAACCAGGACCGAGTAATTTGATCGCTTTTCGTATACCTTTCGATGGGCTACTT 660
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Db      361 CATAATCCAGCAACCAGGACCGAGTAATTTGATCGCTTTTCGTATACCTTTCGATGGGCTACTT 420
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QY      781 TTGGGATTCACAAACGATTAATGTCATGAAACTATATAGACTAATTAAGGCATATTGAT 840
DB      541 TGGGATTCACAAACGATTAATGTCATGAAACTATATAGACTAATTAAGGCATATTGAT 600
QY      841 GAATATGCTGATCACTGTGCAATACGTATATATCGGGGATTAATAATTTTACCGAATCT 900
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QY      901 ACGTATCAAGATTGGATAACATATATATCGATTACGGAGAGACTTAACTTGTATTA 960
DB      661 ACGTATCAAGATTGGATAACATATATATCGATTACGGAGAGACTTAACTTGTATTA 720
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QY      1081 GTAGCTCAATTACCTACTTTTAACTTATGAGAGACGCGCAATTAGAAATCCTCATTTA 1140
DB      841 GTAGCTCAATTACCTACTTTTAACTTATGAGAGACGCGCAATTAGAAATCCTCATTTA 900
QY      1141 TTTGATATATGCAATTAATCTTACAATCTTTACGGATTTGGTTTAGTGTGGAGCAATTTT 1200
DB      901 TTTGATATATGCAATTAATCTTACAATCTTTACGGATTTGGTTTAGTGTGGAGCAATTTT 960
QY      1201 TATTCGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGTAACATACATCTCCT 1260
DB      961 TATTCGGGAGGACATCGAGTAATATCTAGCCTTATAGGAGGTGTAACATACATCTCCT 1020
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1441 GGCACCTCTGTCATTTACAGGACGAGGATTTACAGAGGGGATATCTTCGAGGAATACC 1500
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2101 GCAGATCTGATTTAGAACGACCAAGGGGGTGAATGCCCTGTTTACTTCTTCCAAT 2160
1861 GCAGATCTGATTTAGAACGACCAAGGGGGTGAATGCCCTGTTTACTTCTTCCAAT 1920
2161 CAAATCCGGTAAAAACCGATGACGGATATCATATGATCAAGTATCCATTTAGTG 2220
1921 CAAATCCGGTAAAAACCGATGACGGATATCATATGATCAAGTATCCATTTAGTG 1980
2221 GATTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAATTTGTCGAGAACTCAAA 2280
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2401 GACGTATTTCAAGAGATTTACGTACACTACCGGTACCGTTGATGATGCTATCCAAG 2460
2161 GACGTATTTCAAGAGATTTACGTACACTACCGGTACCGTTGATGATGCTATCCAAG 2220
2461 TATTTATATCAGAAATATAGATGAGTGAATTTAAAGCTTATACCGGTTATGAATTAAGA 2520
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Query Match      89.6%; Score 2429.4; DB 3; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGAGGAGAAATTAATCAAAATCAATGCATACCTTCAATTTTAAAGTAAATCTCTGAAGAA 300
DB 1 ATGAGGAGAAATTAATCAAAATCAATGCATACCTTCAATTTTAAAGTAAATCTCTGAAGAA 60
QY 301 GTACTTTTGGATGGAGACGGATATCAACTGGTAAATCAATTTGATATTTCTCTGTCA 360
DB 61 GTACTTTTGGATGGAGACGGATATCAACTGGTAAATCAATTTGATATTTCTCTGTCA 120
QY 361 CTGTTCAGTTCTCTGTATCACTTTGTACAGGGGGAGGATTTTGTAGTTGATTAATA 420
DB 121 CTGTTCAGTTCTCTGTATCACTTTGTACAGGGGGAGGATTTTGTAGTTGATTAATA 180
QY 421 GATTTGTATGGGGAATAGTTGGCCCTCTCAATGGATGATTTCTAGTACAAATTTGAA 480
DB 181 GATTTGTATGGGGAATAGTTGGCCCTCTCAATGGATGATTTCTAGTACAAATTTGAA 240
QY 481 CAATTAATTAATGAAGAATAGCTGAATTTGTAGTAAAGTAAATTTAAAGATGGAGAGATCT 540
DB 241 CAATTAATTAATGAAGAATAGCTGAATTTGTAGTAAAGTAAATTTAAAGATGGAGAGATCT 300
QY 541 GGATTTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGATGGAGAGATCT 600
DB 301 GGATTTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGATGGAGAGATCT 360

Sequence 1, Application US/09314093
Patent No. 6033874
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettius, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: /09/314,093
APPLICATION NUMBER: US/09/314,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/980,071
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: CDS
LOCATION: 1..3567
US-09-314-093-1
```

RESULT 13
US-09-314-093-1

QY 601 AATAATCCAGCAACCAAGGACCAAGAGTAATGTATCGCTTCGTATATCTTGATGGCTACTT 660
DB 361 AATAATCCAGCAACCAAGGACCAAGAGTAATGTATCGCTTCGTATATCTTGATGGCTACTT 420
QY 661 GAAAGGGACATTCCTTCGTTCCGAATTCCTGGATTTGAAAGTACCCCTTTTATCCGTTTAT 720
DB 421 GAAAGGGACATTCCTTCGTTTCGAATTCCTGGATTTGAAAGTACCCCTTTTATCCGTTTAT 480
QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCCTGAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCCTGAATTTTGGAGAAAGA 540
QY 781 TTGGGATTTGACACGATAAATGTCAATGAAGAACTATAATAGACTAATTAAGGCATATTTGAT 840
DB 541 TTGGGATTTGACACGATAAATGTCAATGAAGAACTATAATAGACTAATTAAGGCATATTTGAT 600
QY 841 GAATATGCTGATCACTGTGCAATAGCTATATTCGGGGATTAATTAATTTTACCGAATCT 900
DB 601 GAATATGCTGATCACTGTGCAATAGCTATATTCGGGGATTAATTAATTTTACCGAATCT 660
QY 901 ACGTATCAAGATTTGGATAACATAATCGATTCAGTACGGAGAGACTTAACATTTGACTGTATTA 960
DB 661 ACGTATCAAGATTTGGATAACATAATCGATTCAGTACGGAGAGACTTAACATTTGACTGTATTA 720
QY 961 GATATCGCGCTTTCTTTCCAACTATGAACAATAGAGATATCCAAATTCAGCCAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTTCCAACTATGAACAATAGAGATATCCAAATTCAGCCAGTTGGT 780
QY 1021 CAACTAACAGGAGAGTTTATACGGACCCATTAATTTAATTTTAAATCCAGTTACAGTCT 1080
DB 781 CAACTAACAGGAGAGTTTATACGGACCCATTAATTTAATTTTAAATCCAGTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTTTTAACTTTATGGAGCAGCGCAATTAAGAAATCCTCAATTTA 1140
DB 841 GTAGCTCAATTAACCTTTTAACTTTATGGAGCAGCGCAATTAAGAAATCCTCAATTTA 900
QY 1141 TTTGATATATGAATAATCTTAACAATCTTTTACGGATTTGGTTAGTGTGGAGCGCAATTTT 1200
DB 901 TTTGATATATGAATAATCTTAACAATCTTTTACGGATTTGGTTAGTGTGGAGCGCAATTTT 960
QY 1201 TATTTGGGAGGACATCGAGTAATATCTAGCTTATAGGAGTGGTAAATCAATCTCTCT 1260
DB 961 TATTTGGGAGGACATCGAGTAATATCTAGCTTATAGGAGTGGTAAATCAATCTCTCT 1020
QY 1261 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAAATGGACCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGCAACAGGAGCTTCAAGATCTTTTAAATGGACCGGTA 1080
QY 1321 TTTAGGACTTTTATCAATTCCTACTTTACGATTTATACGAACTTTGGCCAGCGCACCA 1380
DB 1081 TTTAGGACTTTTATCAATTCCTACTTTACGATTTATACGAACTTTGGCCAGCGCACCA 1140
QY 1381 TTTTAAATTTACGTTGGTGAAGAGTAAATTTTCTACACCTTACAAATAGCTTTAGTAT 1440
DB 1141 TTTTAAATTTACGTTGGTGAAGAGTAAATTTTCTACACCTTACAAATAGCTTTAGTAT 1200
QY 1441 GCAGGAAGAGGTACGTTGATCTTTTAACTTTACCGCTTGGAGTAATAGTGTGCCA 1500
DB 1201 GCAGGAAGAGGTACGTTGATCTTTTAACTTTACCGCTTGGAGTAATAGTGTGCCA 1260
QY 1501 CCTCGGAAAGGATATAGTCAATCGTTTATGTCAATCTTTTGTTCAAAGATCTGGAAACA 1560
DB 1261 CCTCGGAAAGGATATAGTCAATCGTTTATGTCAATCTTTTGTTCAAAGATCTGGAAACA 1320
QY 1561 CCTTTTAACTACGTTAGTATTTTCTTGAACGATCGTAGTGCAATCTCTTCAAT 1620
DB 1321 CCTTTTAACTACGTTAGTATTTTCTTGAACGATCGTAGTGCAATCTCTTCAAT 1380
QY 1621 ACAAATGATCCAGAGAGAAATTAATCAATACCTTTTGTGAAAGGATTTAGGTTGGGG 1680
DB 1381 ACAAATGATCCAGAGAGAAATTAATCAATACCTTTTGTGAAAGGATTTAGGTTGGGG 1440

QY 1681 GGCACCTCTGTCAATTAAGGACCAAGATTTACAGAGGGGATATCTTCCGAAGAAATACC 1740
DB 1441 GGCACCTCTGTCAATTAAGGACCAAGATTTACAGAGGGGATATCTTCCGAAGAAATACC 1500
QY 1741 TTTTGGTGTATTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCCAAAGATACCGT 1800
DB 1501 TTTTGGTGTATTTGTATCTCTCAAGTCAATATTAATTCACCAATTTACCCAAAGATACCGT 1560
QY 1801 TTAAGATTTTCGTTAGCTTCCAGTATAGGATGACAGAGTTATAGTATTAATTAACAGAGCGGCA 1860
DB 1561 TTAAGATTTTCGTTAGCTTCCAGTATAGGATGACAGAGTTATAGTATTAATTAACAGAGCGGCA 1620
QY 1861 TCCAAGAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTTCCAGAAAACTATGGAATA 1920
DB 1621 TCCAAGAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTTCCAGAAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTTAGACATCTAGACATTAAGATATACCGATTTTAGTAATCTTTTTCATTT 1980
DB 1681 GGGGAGAACTTAACTTAGACATCTAGACATTAAGATATACCGATTTTAGTAATCTTTTTCATTT 1740
QY 1981 AGAGCTAATCCAGATATTAATTTGGGATTAAGTGAACCACTCTATTTGGTGCAGTTCCTATT 2040
DB 1741 AGAGCTAATCCAGATATTAATTTGGGATTAAGTGAACCACTCTATTTGGTGCAGTTCCTATT 1800
QY 2041 AGTAGCTGTAACTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100
DB 1801 AGTAGCTGTAACTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 1860
QY 2101 GCAGAACTCTGATTTTAAAGAGACCAAAAGCGGCGTGAATGCGCTGTTTACTTCTTCCAAAT 2160
DB 1861 GCAGAACTCTGATTTTAAAGAGACCAAAAGCGGCGTGAATGCGCTGTTTACTTCTTCCAAAT 1920
QY 2161 CAAATCGCGTTAAAAACCGATGTGACGATTAATCATATTTGATCAAGTATCCAAATTTAGTG 2220
DB 1921 CAAATCGCGTTAAAAACCGATGTGACGATTAATCATATTTGATCAAGTATCCAAATTTAGTG 1980
QY 2221 GATTTGTTATCAGATGAATTTTGTCTGGATGAAACCGAGAAATTTGTCGAGAAAGTCAAA 2280
DB 1981 GATTTGTTATCAGATGAATTTTGTCTGGATGAAACCGAGAAATTTGTCGAGAAAGTCAAA 2040
QY 2281 CATCGAAGCGACTCAGTGATGAGCGGAATTTTACTTCAAGATCCAAATCTTCAGAGGGATC 2340
DB 2041 CATCGAAGCGACTCAGTGATGAGCGGAATTTTACTTCAAGATCCAAATCTTCAGAGGGATC 2100
QY 2341 AATAGACAACCAAGACCGCTGGCTGGAGAGAGTACAGATATTTACCATCCAAAGAGAGAT 2400
DB 2101 AATAGACAACCAAGACCGCTGGCTGGAGAGAGTACAGATATTTACCATCCAAAGAGAGAT 2160
QY 2401 GACGTATTTCAAAGAGAAATTTACGTCACTACCGGCTACCGTTGATGAGTGTATCCAAAG 2460
DB 2161 GACGTATTTCAAAGAGAAATTTACGTCACTACCGGCTACCGTTGATGAGTGTATCCAAAG 2220
QY 2461 TATTTATATCAGAAAAATAGTGTGGAATTTAAAGCTTATACCGTTATGAATTAAGA 2520
DB 2221 TATTTATATCAGAAAAATAGTGTGGAATTTAAAGCTTATACCGTTATGAATTAAGA 2280
QY 2521 GGGTATATCGAAGATAGTCAAGACTTTAGAAATCTATTTGATCGCGTACAAATCGAAAAAC 2580
DB 2281 GGGTATATCGAAGATAGTCAAGACTTTAGAAATCTATTTGATCGCGTACAAATCGAAAAAC 2340
QY 2581 GAAATAGTAAATTTGCCAGGACCGGTTCTTTATGGCGCTTTTACGCCAAAGTCCAATC 2640
DB 2341 GAAATAGTAAATTTGCCAGGACCGGTTCTTTATGGCGCTTTTACGCCAAAGTCCAATC 2400
QY 2641 GGAAGTGTGAGAAACCGAATCGATGCGGCGCAACCTTGAATGAATCTCTGATCTAGAT 2700
DB 2401 GGAAGTGTGAGAAACCGAATCGATGCGGCGCAACCTTGAATGAATCTCTGATCTAGAT 2460
QY 2701 TGTTCCTGCAG 2711
DB 2461 TGTTCCTGCAG 2471

us-09-918-485-1.rni

Wed Oct 15 11:56:11 2003

RESULT 14
US-09-314-093-11
Sequence 11, Application US/09314093
Patent No. 6033874
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettles, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/980,071
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3567

Query Match 89.6%; Score 2429.4; DB 3; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 241 ATGGAGGAAATTAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAGAA 300
DB 1 ATGGAGGAAATTAATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCCTGAGAA 60
QY 301 GTACTTTTGGATGGAGAACGATATCAACTGGTAATTAATCAATGTAATTTCTGTGCA 360
DB 61 GTACTTTTGGATGGAGAACGATATCAACTGGTAATTAATCAATGTAATTTCTGTGCA 120
QY 361 CTGTTTCAGTTTCTGTTATCTAACTTTGTACACGAGGAGGATTTTGTAGTTGGATTAATA 420
DB 121 CTGTTTCAGTTTCTGTTATCTAACTTTGTACACGAGGAGGATTTTGTAGTTGGATTAATA 180
QY 421 GATTTTGTGGGATAGTTGGCCCTTCTCAATGGATGATTTCTAGTCAAAATGAA 480
DB 181 GATTTTGTGGGATAGTTGGCCCTTCTCAATGGATGATTTCTAGTCAAAATGAA 240
QY 481 CAATTAATTAAGGAATAGCTGATTTGCTAGGAATGCTGATTTCTCTAAATTTAGAA 540
DB 241 CAATTAATTAAGGAATAGCTGATTTGCTAGGAATGCTGATTTCTCTAAATTTAGAA 300
QY 541 GGATTAGGAAACAAATTCATATATATGTGGAGCAATTTAAAGAAATGGGAAGATCCT 600

DB 301 GGATTAGGAAACAAATTCATATATATGTGGAGCAATTTAAAGAAATGGGAAGATCC 360
QY 601 AATATCCAGCAACAGGACAGAGTAATGATCGCTTTCGTATATCGTATGAGTGGCTACTT 660
DB 361 CATATCCAGCAACAGGACAGAGTAATGATCGCTTTCGTATATCGTATGAGTGGCTACTT 420
QY 661 GAAGGACATTCCTCGTTTCGAATTTCTGGATTTGAAAGTACCCCTTTATCCGTTTAT 720
DB 421 GAAGGACATTCCTCGTTTCGAATTTCTGGATTTGAAAGTACCCCTTTATCCGTTTAT 480
QY 721 GCTCAAGGCGCATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAG 780
DB 481 GCTCAAGGCGCATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAG 540
QY 781 TTGGATTTGACACGATTAATGTCAATGAAATCTATTAATAGACTAATTAGGCATATTGAT 840
DB 541 TGGGATTTGACACGATTAATGTCAATGAAATCTATTAATAGACTAATTAGGCATATTGAT 600
QY 841 GAATATGCTGATCACTGTCGAATAGCTATATCGGGATTTAAATAATTTACCGAAATCT 900
DB 601 GAATATGCTGATCACTGTCGAATAGCTATTAATCGGGATTTAAATAATTTACCGAAATCT 660
QY 901 ACCTATCAAGATTGGATAACATATATCGATTCGAGAGACTTAACATTCGACTGTATTA 960
DB 661 ACCTATCAAGATTGGATAACATATATCGATTCGAGAGACTTAACATTCGACTGTATTA 720
QY 961 GATATCGCGCTTTCTTCCAAATAGATAGAGATATCCAAATTCAGCCAGTTGGT 1020
DB 721 GATATCGCGCTTTCTTCCAAATAGATAGAGATATCCAAATTCAGCCAGTTGGT 780
QY 1021 CAACTAACAGGAAAGTTTATACGACCCATTAATTTTAAATCCAGTTCAGTCT 1080
DB 781 CAACTAACAGGAAAGTTTATACGACCCATTAATTTTAAATCCAGTTCAGTCT 840
QY 1081 GTAGTCAATTTACCTACTTTTAAAGCTTTTACGAGAGCGCAATTTAGTAATCCTCAATTA 1140
DB 841 GTAGTCAATTTACCTACTTTTAAAGCTTTTACGAGAGCGCAATTTAGTAATCCTCAATTA 900
QY 1141 TTTGATATTTGAATAATCTTTACAAATCTTTACGAGATGTTTGTAGTTGGAGCGAATTT 1200
DB 901 TTTGATATTTGAATAATCTTTACAAATCTTTACGAGATGTTTGTAGTTGGAGCGAATTT 960
QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGAGTGGTGAACATATCTCT 1260
DB 961 TATTGGGAGGACATCGAGTAATATCTAGCTTTATAGAGTGGTGAACATATCTCT 1020
QY 1261 ATATATGGAAGAGAGGCGAACAGGAGCTTCAAGATCTTTTACGAGTGGTGAACATATCTCT 1320
DB 1021 ATATATGGAAGAGAGGCGAACAGGAGCTTCAAGATCTTTTACGAGTGGTGAACATATCTCT 1080
QY 1321 TTTAGGACTTTTATCAATTTCTACTTTTACGATTTTACAGCAACCTTCCAGCGCCACAT 1380
DB 1081 TTTAGGACTTTTATCAATTTCTACTTTTACGATTTTACAGCAACCTTCCAGCGCCACCA 1140
QY 1381 TTTTATTTAGCTGGTGAAGGATGAGAAATTTTACACCTTACACCTTACAAATAGCTTTAGCTAT 1440
DB 1141 TTTTATTTAGCTGGTGAAGGATGAGAAATTTTACACCTTACACCTTACAAATAGCTTTAGCTAT 1200
QY 1441 GCAGAGAGGATAGCTGATTTCTTAACTGAATTTACCGCTGAGGATTAATAGTGGCA 1500
DB 1201 CGAGAGAGGATAGCTGATTTCTTAACTGAATTTACCGCTGAGGATTAATAGTGGCA 1260
QY 1501 CTTCCGAGGATAGCTGATTTCTTAACTGAATTTTGTCTGCAACTTTTGTTCAAAAGATTCGGAACA 1560
DB 1261 CTTCCGAGGATAGCTGATTTCTTAACTGAATTTTGTCTGCAACTTTTGTTCAAAAGATTCGGAACA 1320
QY 1561 CTTTATTTAACTGCTGATTTCTTGTGAGCGATCTAGTGAACCTTTTACAAAT 1620
DB 1321 CTTTATTTAACTGCTGATTTCTTGTGAGCGATCTAGTGAACCTTTTACAAAT 1380
QY 1621 ACATTTGATCCGAGAGATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1680

Db 1381 ACAATTGATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGGATTTAGATTTGGGG 1440

Qy 1681 GGCACCTCTCTCATTACAGGACAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACC 1740

Db 1441 GGCACCTCTCTCATTACAGGACAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACC 1500

Qy 1741 TTTGGTGATTTTGTATCTCTACAGTCAATATTAATTTACCAATTTACCCAAAGATACCGT 1800

Db 1501 TTTGGTGATTTTGTATCTCTACAGTCAATATTAATTTACCAATTTACCCAAAGATACCGT 1560

Qy 1801 TTAAGATTTTCTTACGCTTCCAGTGGGATGCGAGTATATAGTATTAATTAACAGGAGGGCA 1860

Db 1561 TTAAGATTTTCTTACGCTTCCAGTGGGATGCGAGTATATAGTATTAATTAACAGGAGGGCA 1620

Qy 1861 TCCACAGGAGTGGGAGCCCAAGTTAGTGTAGATATGCTCTTCAGAAAATCTATGGAATA 1920

Db 1621 TCCACAGGAGTGGGAGCCCAAGTTAGTGTAGATATGCTCTTCAGAAAATCTATGGAATA 1680

Qy 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTATCTTTTCAATTT 1980

Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTATCTTTTCAATTT 1740

Qy 1981 AGAGCTAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTTGTCGAGGTTCTATT 2040

Db 1741 AGAGCTAATCCAGATATAATTTGGGATAAGTGAACAACTCTATTTGTCGAGGTTCTATT 1800

Qy 2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTACAGATGCAACATTTGAA 2100

Db 1801 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTACAGATGCAACATTTGAA 1860

Qy 2101 GCAGATCTGATTTAGAAAGAGCACAAAGCGCGTGAATGCGCTGTTTACTTCTTCCAAT 2160

Db 1861 GCAGATCTGATTTAGAAAGAGCACAAAGCGCGTGAATGCGCTGTTTACTTCTTCCAAT 1920

Qy 2161 CAAATCGGGTAAAAACCGATGTGACGGATATCATATTGATCAAGTATCCATTTAGTG 2220

Db 1921 CAAATCGGGTAAAAACCGATGTGACGGATATCATATTGATCAAGTATCCATTTAGTG 1980

Qy 2221 GATTTGTTATCAGATGAATTTTCTGCTGATGAAAGCGAGAAATTTGCGAGAAAGTCAAA 2280

Db 1981 GATTTGTTATCAGATGAATTTTCTGCTGATGAAAGCGAGAAATTTGCGAGAAAGTCAAA 2040

Qy 2281 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2340

Db 2041 CATGCAAGGACTCAGTATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGATC 2100

Qy 2341 AATAGACAAACCGACCGTGGCTGGAGGAAGTACAGATATTTACCATCCAGAGGAGAT 2400

Db 2101 AATAGACAAACCGACCGTGGCTGGAGGAAGTACAGATATTTACCATCCAGAGGAGAT 2160

Qy 2401 GAGCTATTCAAAGAGAAATACGTACACTACCGGTACCGTTGATGAGTGCTATCCAAG 2460

Db 2161 GAGCTATTCAAAGAGAAATACGTACACTACCGGTACCGTTGATGAGTGCTATCCAAG 2220

Qy 2461 TATTTATACAGAAAATAGATAGTGCAGAAATTTAAAGCTTATACCGTTATGAATTAAGA 2520

Db 2221 TATTTATACAGAAAATAGATAGTGCAGAAATTTAAAGCTTATACCGTTATGAATTAAGA 2280

Qy 2521 GGTATATCGAGATGATCAAGCTTTAGAAATCTATTTGATCGCGTACAAATGCAAAACAC 2580

Db 2281 GGTATATCGAGATGATCAAGCTTTAGAAATCTATTTGATCGCGTACAAATGCAAAACAC 2340

Qy 2581 GAAATAGTAAATGTGCGAGCGCGGTCTCTTATGCGCGCTTTACGCCCAAAAGTCAAAATC 2640

Db 2341 GAAATAGTAAATGTGCGAGCGCGGTCTCTTATGCGCGCTTTACGCCCAAAAGTCAAAATC 2400

Qy 2641 GGAAGTGTGGAGAACCGAATCGATGCGGCCACACTTTGAATTTGAATCTGATCTAGAT 2700

Db 2401 GGAAGTGTGGAGAACCGAATCGATGCGGCCACACTTTGAATTTGAATCTGATCTAGAT 2460

Qy 2701 TGTCTCTGCAG 2711

Db 2461 TGTCTCTGCAG 2471

RESULT 15

US-08-933-891-5

Sequence 5, Application US/08933891

Patent No. 6096708

GENERAL INFORMATION:

APPLICANT: Payne, Jewel M.

APPLICANT: Sick, August J.

TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate

TITLE OF INVENTION: Active Against Lepidopteran Peats, and Genes Encoding

TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,891

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/356,034

FILING DATE:

APPLICATION NUMBER: US/08/210,110

FILING DATE:

APPLICATION NUMBER: 07/865,168

FILING DATE: 09-APR-92

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/451,261

FILING DATE: 14-DEC-89

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/371,955

FILING DATE: 27-JUN-89

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, Roman

REGISTRATION NUMBER: 21,023

REFERENCE/DOCKET NUMBER: MA43.C1.D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904)375-8100

TELEFAX: (904)372-5800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 3567 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: BACILLUS THURINGIENSIS

STRAIN: AIZAWAI

INDIVIDUAL ISOLATE: PS811

IMMEDIATE SOURCE:

LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK

CLONE: 811B2

US-08-933-891-5

Query Match 89.6%; Score 2429.4; DB 3; Length 3567;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 241 ATGAGGAGAAATCAATCAAAATCAATGTCATACCTTCAATTTGTTTAAGTAATCTCGAAGAA 300

|||||

1 ATGGAGAAATTAATCAAAATCAATGCATACCTTAACATTTGTTAAAGTAATCCTGAAGAA 60
301 GTACTTTTGGATGGAGAAACGGATATCAACTGGTAATTTACTCAATTTGATTTCTCTGTCA 360
61 GTACTTTTGGATGGAGAAACGGATATCAACTGGTAATTTACTCAATTTGATTTCTCTGTCA 120
361 CTTGTTTCACTGTTCTGTTATCTAACTTTGTACACGGGGAGGATTTTGTAGTTGGATTAATA 420
121 CTTGTTTCACTGTTCTGTTATCTAACTTTGTACACGGGGAGGATTTTGTAGTTGGATTAATA 480
421 GATTTTGTATGGGAATAGTTGGCCCTTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
181 GATTTTGTATGGGAATAGTTGGCCCTTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240
481 CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGTAATTTCTTAATTTAGAA 540
241 CAATTAATTAATGAAGAAATAGCTGAATTTGCTAGGAATGCTGTAATTTCTTAATTTAGAA 300
541 GGATTTAGGAACAAATTTCAATATATATATGTGAAGCAATTTAAAGAAATGGGAAGATCCT 600
301 GGATTTAGGAACAAATTTCAATATATATGTGAAGCAATTTAAAGAAATGGGAAGATCCT 360
601 AATTAATCCAGCAACGAGGACGAGTAATTTGATCGCTTTGCTATCTTGTATGATGGCTACTT 660
361 AATTAATCCAGCAACGAGGACGAGTAATTTGATCGCTTTGCTATCTTGTATGATGGCTACTT 420
661 GAAAGGACATTCCTTTGTTGGAATTTCTGGAATTTCTGGAATTTCTGGAATTTCTGGAATTT 720
421 GAAAGGACATTCCTTTGTTGGAATTTCTGGAATTTCTGGAATTTCTGGAATTTCTGGAATTT 480
721 GCTCAAGCGGCAATCTGATCTAGCTATTAATGAAGATCTGTTGAATTTTGGGAAGA 780
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Job time : 242 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2003, 22:40:15 ; Search time 855 Seconds
(without alignments)
8559.271 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711
Sequence: 1 AGCTTCAATAGAACTCAA.....GATCTAGATTGTTCTGCGAC 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2695	99.4	2711	9 AAN81949	Encodes delta endo
2	2688.2	99.2	2711	9 AAN81242	Sequence of a 3kb
3	2664	98.3	3923	12 AAQ10229	Sequence encoding
4	2432.6	89.7	3567	12 AAQ10181	Lepidopteran-activ
5	2431	89.7	3567	16 AAQ80646	CryIC gene. Bacil
6	2429.4	89.6	3567	14 AAQ47294	Delta endotoxin ge
7	2429.4	89.6	3567	19 AAV27848	DNA encoding a mut
8	2429.4	89.6	3567	19 AAV27843	DNA encoding a mut

9	2429.4	89.6	3567	20 AAX80039	B. thuringiensis c
10	2429.4	89.6	3567	20 AAX80019	B. thuringiensis c
11	2429.4	89.6	3567	21 AAA08144	Bacillus thuringie
12	2429.4	89.6	3567	21 AAA08149	Bacillus thuringie
13	2429.4	89.6	3567	24 AAD44210	Bacillus thuringie
14	2429.4	89.6	3567	24 AAD44215	Bacillus thuringie
15	2429.4	89.6	3567	24 ABS70781	B. thuringiensis D
16	2429.4	89.6	3567	24 ABS70786	B. thuringiensis D
17	2427.8	89.6	3567	19 AAV27845	DNA encoding a mut
18	2427.8	89.6	3567	19 AAV27847	DNA encoding a mut
19	2427.8	89.6	3567	19 AAV27844	DNA encoding a mut
20	2427.8	89.6	3567	20 AAX80036	B. thuringiensis c
21	2427.8	89.6	3567	20 AAX80038	B. thuringiensis c
22	2427.8	89.6	3567	20 AAX80020	B. thuringiensis c
23	2427.8	89.6	3567	21 AAA08145	Bacillus thuringie
24	2427.8	89.6	3567	21 AAA08146	Bacillus thuringie
25	2427.8	89.6	3567	21 AAA08148	Bacillus thuringie
26	2427.8	89.6	3567	24 AAD44211	Bacillus thuringie
27	2427.8	89.6	3567	24 AAD44212	Bacillus thuringie
28	2427.8	89.6	3567	24 AAD44214	Bacillus thuringie
29	2427.8	89.6	3567	24 ABS70782	B. thuringiensis D
30	2427.8	89.6	3567	24 ABS70783	B. thuringiensis D
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35	2426.2	89.5	3567	24 AAD44213	Bacillus thuringie
36	2426.2	89.5	3567	24 ABS70784	B. thuringiensis D
37	2421.4	89.3	3567	22 AAS08951	Bacillus thuringie
38	2419.8	89.3	3567	19 AAV27863	DNA encoding a mut
39	2419.8	89.3	3567	20 AAX80004	EG12111 crystal pr
40	2419.8	89.3	3567	21 AAA08166	Bacillus thuringie
41	2419.8	89.3	3567	24 AAD44232	Bacillus thuringie
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43	2418.2	89.2	3567	19 AAV27864	DNA encoding a mut
44	2418.2	89.2	3567	20 AAX80005	EG12121 crystal pr
45	2418.2	89.2	3567	21 AAA08167	Bacillus thuringie

ALIGNMENTS

RESULT 1	
AAN81949	
ID AAN81949 standard; cDNA; 2711 BP.	
XX	
AC AAN81949;	
XX	
DT 25-MAR-2003 (updated)	
DT 23-OCT-1990 (first entry)	
XX	
DE Encodes delta endotoxin active against Lepidoptera larvae.	
XX	
KW Lepidoptera larvae; insecticide; Bacillus thuringiensis;	
KW Spodoptera littoralis; ss.	
XX	
OS synthetic.	
XX	
FH Key	Location/Qualifiers
FT CDS	241..2711
FT	/*tag= a
FT	/product=insecticidal polypeptide
XX	
PN WO8809812-A.	
XX	
PD 15-DEC-1988.	
PF	
XX 09-JUN-1988; 88WO-FR00292.	
PR	
XX 10-JUN-1987; 87FR-0008090.	
PR	
XX 06-MAY-1988; 88EP-0401121.	
PA (INST) INST PASTEUR.	

PA (INRG) INST NAT RECH AGRONOMIQ.
 XX Sanchis V, Lereclus D, Menou G;
 XX WPI: 1988-368627/51.
 XX P-PSDB; AAP81502.
 DR New nucleotide sequences encoding new polypeptide -
 XX with selective action against lepidopteran larvae esp Spodoptera
 PT littoralis
 XX Claim 9, Page 47; 65pp; French.
 XX The sequence is derived from a 3kb HindIII-PstI fragment of
 CC Bacillus thuringiensis. Recombinant sequences can also be
 CC constructed from 2 diff strains of B. thuringiensis. The sequence
 CC between bases 50 to 95 is claimed separately as this encodes at
 CC least a part of the N-terminal region of an insecticidal
 CC polypeptide. There is a variable nucleotide at posn 611 which is C
 CC in the sequence given here but which is A in the shorter sequence.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX SQ Sequence 2711 BP; 877 A; 442 C; 560 G; 832 T; 0 other;
 Query Match 99.4%; Score 2695; DB 9; Length 2711;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2701; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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 DB 1 AAGCTTCAATAGATCTCAATCTCGATGACTGCTGCTAGTCTTTTATATCTGCTACTTG 60
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 DB 361 CTTGTTTCACTTTCTGTTATCTTAATTTGTACCAGGGGAGGATTTTAAAGTTGGAATTA 420
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 Db 2581 GAAATAGTAAATGTGCGAGCAGCGGTTCCTTATGGCGGCTTTTACGCCCAAGTCCAAATC 2640
 QY 2641 GGAAGTGTGGAGAACCGGAATCGATGCGGCCACACCTTTGAAATGGAATCCTGATCTAGAT 2700
 Db 2641 GGAAGTGTGGAGAACCGGAATCGATGCGGCCACACCTTTGAAATGGAATCCTGATCTAGAT 2700
 QY 2701 TGTTCCTGCAG 2711
 Db 2701 TGTTCCTGCAG 2711

RESULT 2

AAN81242

ID AAN81242 standard; DNA; 2711 BP.

XX

AC AAN81242;
 XX 25-MAR-2003 (updated)
 DT 30-OCT-1990 (first entry)
 XX
 DE Sequence of a 3kb Hind III-Pst I fragment of *Bacillus thuringiensis* (BT)
 DE strain aizawai 7-29 and entomocidus 6-01.
 XX
 KW Microbial insecticide; pesticide; bacterium; Noctuellae;
 KW Spodoptera littoralis; Mamestra brassicae; ss.
 XX
 OS *Bacillus thuringiensis*.
 XX
 PN EP295156-A.
 XX 14-DEC-1988.
 PD
 XX 06-MAY-1988; 88EP-0401121.
 PF
 XX 10-JUN-1987; 87FR-0008090.
 PR
 XX (INSP) INST PASTEUR.
 PA (CNES) CENT NAT RECH SCI.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX
 Sanchis V, Lereclus D, Menou G, Lecadet MM, Martouret D, Dedonder R;
 XX WPI; 1988-355565/50.
 DR
 XX New DNA sequences encoding insecticidal polypeptide -
 PT with specific activity against lepidoptera larvae esp.
 PT Spodoptera littoralis
 XX
 PS Claim 9; Pages 23-25; 37pp; French.
 XX
 CC It can hybridise with 3 specified probes from the gene of BT crystal
 CC protein. It is particularly derived from the BT, or by in vitro genetic
 CC recombination of DNA fragments from 2 different BT strains, esp. aizawai
 CC 7-29 deposited as CNM I-661 or I-660, resp. It encodes at least part of
 CC the N-terminal region of a polypeptide which is specifically toxic for
 CC lepidopteran larvae of family Noctuellae (esp. Spodoptera littoralis).
 CC It can be used to express polypeptides which are used as insecticides
 CC (against S. littoralis or Mamestra brassicae). may also be incorporated
 CC directly in littoralis or micro-organisms, pref. Pseudomonas, Azospirillum
 CC or Rhizobium, which live in the plant environment.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 2711 BP; 873 A; 443 C; 563 G; 831 T; 1 other;

Query Match 99.2%; Score 2688.2; DB 9; Length 2711;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2696; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 2 AGCTTCAATAGATCTCAAAATCTCGATGCTTGTAGTCTTTTAACTACTGTCTACTGA 61
 Db 2 AGCTTCAATAGATCTCAAAATCTCGATGCTTGTAGTCTTTTAACTACTGTCTACTGA 61
 QY 62 CAGGGGTAGGACATAATCGGTCATTTTAAATATGGGCGATATATGATATTTTATAA 121
 Db 62 CAGGGGTAGGACATAATCGGTCATTTTAAATATGGGCGATATATGATATTTTATAA 121
 QY 122 ATTTGTTACGTTTTTGTATTTTTCATAAGATGTGTCATATGTTAAATCGTGTAT 181
 Db 122 ATTTGTTACGTTTTTGTATTTTTCATAAGATGTGTCATATGTTAAATCGTGTAT 181
 QY 182 GAAAAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAAAACGGAGTATTTTA 241
 Db 182 GAAAAACAGTATCAAACTATCAGAACTTTGGTAGTTTAAATAAAAAACGGAGTATTTTA 241
 QY 242 TGGAGGAAAAATCAAAATCAATGATCACTTACCAATTTGTTAAGTAACTCTGGAAG 301
 Db 242 TGGAGGAAAAATCAAAATCAATGATCACTTACCAATTTGTTAAGTAACTCTGGAAG 301

QY 302 TACTTTTGGATCGGAACGGATATCAACTGGTAATTAATCTCAATGATATTTCTCTGTCAAC 361
Db |
QY 302 TACTTTTGGATCGGAACGGATATCAACTGGTAATTAATCTCAATGATATTTCTCTGTCAAC 361
Db |
QY 362 TTGTTTCAGTTTCTCGTATCTAACTTTGTACACAGGGAGGATTTTGTAGTTGATTAATAG 421
Db |
QY 362 TTGTTTCAGTTTCTCGTATCTAACTTTGTACACAGGGAGGATTTTGTAGTTGATTAATAG 421
Db |
QY 422 ATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGATGCAATTTGTACCAATTCGAAC 481
Db |
QY 422 ATTTTGTATGGGGAATAGTTGGCCCTTCTCAATGGATGCAATTTGTACCAATTCGAAC 481
Db |
QY 482 AATTAATTAATGAAGAATAGCTGAATTTGTAGGAATGCTGCTATTTGCTTAATTTAGAG 541
Db |
QY 482 AATTAATTAATGAAGAATAGCTGAATTTGTAGGAATGCTGCTATTTGCTTAATTTAGAG 541
Db |
QY 542 GATTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGAACTCTA 601
Db |
QY 542 GATTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGAACTCTA 601
Db |
QY 602 ATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGCTACTTG 661
Db |
QY 602 ATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTTCGTATATCTTGATGGCTACTTG 661
Db |
QY 662 AAAGGGACATTCCTCGTTTCGAAATTTCTGGAATTTTGAAGTACCCCTTTTATCCGTTATG 721
Db |
QY 662 AAAGGGACATTCCTCGTTTCGAAATTTCTGGAATTTTGAAGTACCCCTTTTATCCGTTATG 721
Db |
QY 722 CTCAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGGAAGAAGAT 781
Db |
QY 722 CTCAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGGAAGAAGAT 781
Db |
QY 782 TGGGATTTGACACGATTAATGTGAATGAACCTAATTAAGACTAATTTAGGCAATTTGATG 841
Db |
QY 782 TGGGATTTGACACGATTAATGTGAATGAACCTAATTAAGACTAATTTAGGCAATTTGATG 841
Db |
QY 842 AATATGCTGATCACTGTGCAATACGTAATATCGGGGATTAATTAATTTACCGAATCTA 901
Db |
QY 842 AATATGCTGATCACTGTGCAATACGTAATATCGGGGATTAATTAATTTACCGAATCTA 901
Db |
QY 902 CQTATCAAGATTTGGATACATATAATCGATTTACGGAGAGACTTAACATTCATGCTATTAG 961
Db |
QY 902 CQTATCAAGATTTGGATACATATAATCGATTTACGGAGAGACTTAACATTCATGCTATTAG 961
Db |
QY 962 ATATCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATTCMAATTCAGCCAGTTGGTC 1021
Db |
QY 962 ATATCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATTCMAATTCAGCCAGTTGGTC 1021
Db |
QY 1022 AACTAAACAAGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCTG 1081
Db |
QY 1022 AACTAAACAAGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCTG 1081
Db |
QY 1082 TAGCTCAATTAACCTTTTAACTGTTATGGAGAGAGCGCAATTAGAAATCTCTCAATTTAT 1141
Db |
QY 1082 TAGCTCAATTAACCTTTTAACTGTTATGGAGAGAGCGCAATTAGAAATCTCTCAATTTAT 1141
Db |
QY 1142 TTGATATATTAATTAATCTTAATCTTAATCTTAAGGATTTGTTAGTTGGAGCGCAATTTT 1201
Db |
QY 1142 TTGATATATTAATTAATCTTAATCTTAATCTTAAGGATTTGTTAGTTGGAGCGCAATTTT 1201
Db |
QY 1202 ATTTGGGAGGACATCGAGTAATATCTAGCTTATAGAGGTCGTAACATTAACATCTCTA 1261
Db |
QY 1202 ATTTGGGAGGACATCGAGTAATATCTAGCTTATAGAGGTCGTAACATTAACATCTCTA 1261
Db |
QY 1262 TATATGGAAGAGAGCGGACAGGAGCCCTCCAGATCTTACTTTTAAATGGACCGGTAT 1321
Db |
QY 1262 TATATGGAAGAGAGCGGACAGGAGCCCTCCAGATCTTACTTTTAAATGGACCGGTAT 1321
Db |
QY 1322 TTAGGACTTTTATCAATTTCTTATCTTTATTAAGCAATCTTGCCAGGCGCACATTT 1381
Db |
QY 1322 TTAGGACTTTTATCAATTTCTTATCTTTTATTAAGCAATCTTGCCAGGCGCACATTT 1381
Db |
QY 1382 TTAATTTACGTCGTGTAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTATG 1441

Db |
QY 1382 TTAATTTACGTCGTGTAAGGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTATG 1441
Db |
QY 1442 CAGGAAGAGTAGACGCTTTGATTTCTTTAACTGAATTTACCGCTGAGGATTAATAGTGTCCAC 1501
Db |
QY 1442 CAGGAAGAGTAGACGCTTTGATTTCTTTAACTGAATTTACCGCTGAGGATTAATAGTGTCCAC 1501
Db |
QY 1502 CTCGCGAAGGATATAGTCACTGTTTATGTCTCAACACTTTTGTTCAGAGATCTCGAACAC 1561
Db |
QY 1502 CTCGCGAAGGATATAGTCACTGTTTATGTCTCAACACTTTTGTTCAGAGATCTCGAACAC 1561
Db |
QY 1562 CTTTTTTTACAACTGCTGTAGTATTTCTTTGGACGCACTCTTACCAATA 1621
Db |
QY 1562 CTTTTTTTACAACTGCTGTAGTATTTCTTTGGACGCACTCTTACCAATA 1621
Db |
QY 1622 CAATTCATCCAGAGAGATTAATCAATACCTTTTAGTGAAGGATTTAGAGTTGGGGGG 1681
Db |
QY 1622 CAATTCATCCAGAGAGATTAATCAATACCTTTTAGTGAAGGATTTAGAGTTGGGGGG 1681
Db |
QY 1682 GCACCTCTGCTCAATTACAGGACAGGATTTACAGGAGGGGATATCTTCCGAAGATACCT 1741
Db |
QY 1682 GCACCTCTGCTCAATTACAGGACAGGATTTACAGGAGGGGATATCTTCCGAAGATACCT 1741
Db |
QY 1742 TTGGTGATTTGTATCTCAAGTCAATTAATTAATTTACCAATTTACCAAGATACCTTT 1801
Db |
QY 1742 TTGGTGATTTGTATCTCAAGTCAATTAATTAATTTACCAATTTACCAAGATACCTTT 1801
Db |
QY 1802 TAAAGATTTCTGTTTACGCTTTCCAGTAGGATGCAAGATTTATAGTATTTAAACAGAGCGGAT 1861
Db |
QY 1802 TAAAGATTTCTGTTTACGCTTTCCAGTAGGATGCAAGATTTATAGTATTTAAACAGAGCGGAT 1861
Db |
QY 1862 CCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAACTATGGAATAG 1921
Db |
QY 1862 CCACAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAAACTATGGAATAG 1921
Db |
QY 1922 GGGAGAACTTTAACTCTAGAACATTTAGATATACCGATTTTAGTAATCTCTTTTCAATTA 1981
Db |
QY 1922 GGGAGAACTTTAACTCTAGAACATTTAGATATACCGATTTTAGTAATCTCTTTTCAATTA 1981
Db |
QY 1982 GAGCTAATCCAGATATAATTTGGGATAAGTGAACACCTCTATTTGGTGAGAGTCTATTA 2041
Db |
QY 1982 GAGCTAATCCAGATATAATTTGGGATAAGTGAACACCTCTATTTGGTGAGAGTCTATTA 2041
Db |
QY 2042 GTAGCGTGAACCTTTATATAGATAAATTTGAAATTTTCTAGAGAGATGCAATTTGAAG 2101
Db |
QY 2042 GTAGCGTGAACCTTTATATAGATAAATTTGAAATTTTCTAGAGAGATGCAATTTGAAG 2101
Db |
QY 2102 CAGATCTGATTTAGAAAGACCAAAAGCGCTGAATGCCCTGTTTACTTCTTCCAATC 2161
Db |
QY 2102 CAGATCTGATTTAGAAAGACCAAAAGCGCTGAATGCCCTGTTTACTTCTTCCAATC 2161
Db |
QY 2162 AAATCGGTTTAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2221
Db |
QY 2162 AAATCGGTTTAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2221
Db |
QY 2222 ATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAATTTCTCGAGAAAGTCAAAAC 2281
Db |
QY 2222 ATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAATTTCTCGAGAAAGTCAAAAC 2281
Db |
QY 2282 ATGCGAAGCGACTCAGTGAATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATCA 2341
Db |
QY 2282 ATGCGAAGCGACTCAGTGAATGAGCGGAATTTACTTCAAGATCCAAACTTCAGAGGATCA 2341
Db |
QY 2342 ATAGACAAACAGAGCGTGGCTGGAGAGGAAGTACAGATTTACCATCCAAAGGAGAGATG 2401
Db |
QY 2342 ATAGACAAACAGAGCGTGGCTGGAGAGGAAGTACAGATTTACCATCCAAAGGAGAGATG 2401
Db |
QY 2402 AGGTATTTCAAGAGAAATTAAGTCACTACCTACCGGTTACCGTTGATGAGTGTCTTCCAACT 2461
Db |
QY 2402 AGGTATTTCAAGAGAAATTAAGTCACTACCTACCGGTTACCGTTGATGAGTGTCTTCCAACT 2461
Db |
QY 2462 ATTTATATCAGAAATAGATGATGCGAAATTTAAAGCTTTATACCGTTTATGAATTAAGAG 2521

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Db      2462 ATTATATCAGAAATAGATGAGTCGAAATTAAGCTTATACCGTTATGAATTAAGAG 2521
QY      2522 GGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGTATCGGTACAAATGCAAAACACG 2581
Db      2522 GGTATATCGAAGATAGTCAAGACTTAGAAATCTATTGTATCGGTACAAATGCAAAACACG 2581
QY      2582 AAATAGTAAATGTGCGAGCACGGGTTCTTATGCGCGCTTTTCAGGCCAAAGTCCAAATCG 2641
Db      2582 AAATAGTAAATGTGCGAGCACGGGTTCTTATGCGCGCTTTTCAGGCCAAAGTCCAAATCG 2641
QY      2642 GAAAGTGTGAGAACCGAATCGATGCGCGCACACCTTGAATCGAATCTGTATCTAGATT 2701
Db      2642 GAAAGTGTGAGAACCGAATCGATGCGCGCACACCTTGAATCGAATCTGTATCTAGATT 2701
QY      2702 GTTCTGCGAG 2711
Db      2702 GTTCTGCGAG 2711

RESULT 3
ID      AAQ10229
XX      AAQ10229 standard; DNA; 3923 BP.
AC      AAQ10229;
XX      25-MAR-2003 (updated)
DT      27-MAR-1991 (first entry)
XX      Sequence encoding insecticidal crystal protein (ICP) entomocidus
DE      HD-110 of gene bt15.
XX      Insecticide; Lepidoptera; Coleoptera; ds.
XX      Bacillus thuringiensis.
XX      Key Location/Qualifiers
FT      CDS 264..3761
XX      /*tag= a
XX      EP408403-A.
XX      16-JAN-1991.
XX      29-MAY-1990; 90EP-0401427.
XX      29-MAY-1990; 90EP-0401427.
XX      31-MAY-1989; 89EP-0401499.
XX      (PLBZ ) PLANT GENETICS SYSTEMS NV.
XX      Vannellaer H, Botterman J, Vanrie J, Joos H;
XX      WPI; 1991-016587/03.
XX      P-PSDB; AAR10193.
XX      Insect-resistant transgenic plant cells - transformed with genes
PT      encoding different non-competitively binding Bacillus
PT      thuringiensis insecticidal proteins
XX      Disclosure; Fig 14; 82pp; English.
XX      Sequence may be used in transformation of crop plants, providing
CC      resistance to insect (esp. lepidoptera and Coleoptera) attack,
CC      without resort to insecticides which incur problems with development
CC      of insect resistance.
CC      (Updated on 25-MAR-2003 to correct PA field.)
CC      (Updated on 25-MAR-2003 to correct PI field.)
XX      Sequence 3923 BP; 1304 A; 636 C; 849 G; 1134 T; 0 other;
SQ      Query Match 98.3%; Score 2664; DB 12; Length 3923;
      Best Local Similarity 99.1%; Pred. No. 0;
      Matches 2679; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY      8 AATAGAACTCAAAATCTCGATGACCTCTTAGTCTTTTTTAATACTGTCTACTTGCACAGGGG 67
Db      1 AATAGAACTCAAAATCTCGATGACCTCTTAGTCTTTTTTAATACTGTCTACTTGCACAGGGG 60
QY      68 TAGGAACATAAATCGGTCAATTTTAAATATGGGCGCATATTTGATATTTTATAAAATTTGT 127
Db      61 TAGGAACATAAATCGGTCAATTTTAAATATGGGCGCATATTTGATATTTTATAAAATTTGT 120
QY      128 TACGTTTTTTTGTATTTTTCATAAGATGTCTATGTATTAATCGTGTATGAATAA 187
Db      121 TACGTTTTTTTGTATTTTTCATAAGATGTCTATGTATTAATCGTGTATGAATAA 180
QY      188 CAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATCGAGG 247
Db      181 CAGTATCAAACTATCAGAACTTTTGTAGTTTAAATAAAAAACGGAGGTATTTTATCGAGG 240
QY      248 AAATANTCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTT 307
Db      241 AAATANTCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAAGTACTTT 300
QY      308 TGGATGGAGAACGATATCAACTGGTAAATTTACTCAATTCATATTTCTCTGTCACCTGTTTC 367
Db      301 TGGATGGAGAACGATATCAACTGGTAAATTTCAATTCATATTTCTCTGTCACCTGTTTC 360
QY      368 AGTTTTCTGTTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGATTAATAGATTTTG 427
Db      361 AGTTTTCTGTTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGATTAATAGATTTTG 420
QY      428 TATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAACAATTA 487
Db      421 TATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAACAATTA 480
QY      488 TTAATGAAGAAGTAGCTGAATTTGCTAGGAATGCTGCTATTCGTAATTTAGAGGATTAG 547
Db      481 TTAATGAAGAAGTAGCTGAATTTGCTAGGAATGCTGCTATTCGTAATTTAGAGGATTAG 540
QY      548 GAAACAAATTTCAATATATATGTGGAAGCAATTTTAAAGAATGGGAAGAAGATCCCTAATAATC 607
Db      541 GAAACAAATTTCAATATATATGTGGAAGCAATTTTAAAGAATGGGAAGAAGATCCCTAATAATC 600
QY      608 CAGCAACGAGGACGAGATTAATGATCGCTTTTCGTATACCTGATGGGCTACTTGAAGGG 667
Db      601 CAGCAACGAGGACGAGATTAATGATCGCTTTTCGTATACCTGATGGGCTACTTGAAGGG 660
QY      668 ACATTTCTTCTGTTTCGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTATGCTCAAG 727
Db      661 ACATTTCTTCTGTTTCGAAATTTCTGGAATTTGAAGTACCCCTTTTATCCGTTATGCTCAAG 720
QY      728 CGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGATTTGGGAT 787
Db      721 CGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGATTTGGGAT 780
QY      788 TGCAACGATAAATGTCATGAATAAATCTATAATAGACTAATTAAGGCATATTTGATGAATATG 847
Db      781 TGCAACGATAAATGTCATGAATAAATCTATAATAGACTAATTAAGGCATATTTGATGAATATG 840
QY      848 CTGATCACTGTGCAAAATCGTATATCGGGGATTAATAATTAATTCGGAATCTAGCTATC 907
Db      841 CTGATCACTGTGCAAAATCGTATATCGGGGATTAATAATTAATTCGGAATCTAGCTATC 900
QY      908 AAGATTGGATAACATATTAATGATTACGAGAGACTTAACATTTGACTGTATTAGATATCG 967
Db      901 AAGATTGGATAACATATTAATGATTACGAGAGACTTAACATTTGACTGTATTAGATATCG 960
QY      968 CGCTTTCTTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGTCAACTAA 1027
Db      961 CGCTTTCTTTCCAAACTATGACAAATAGAGATATCCAAATTCAGCCAGTTGGTCAACTAA 1020
QY      1028 CAAGGAAGTTTATACGGACCCCATTAATTAATTTTAAATCCAGATTACAGTCTGTAGCTC 1087
Db      1021 CAAGGAAGTTTATACGGACCCCATTAATTAATTTTAAATCCAGATTACAGTCTGTAGCTC 1080

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1088	AY	AATTACCTCTTTTAACTTTATGAGAGCAGCGCAATTAGAAATCTCTCAATTTATTTCGATA	1147	Db	2161	GGTTAAAAACCGATGTGACGGGATTTATCATATTGATCAGATATCCAAATTTAGTGTGAT	2220
1089	Db	AATTACCTCTTTTAACTTTATGAGAGCAGCGCAATTAGAAATCTCTCAATTTATTTCGATA	1140	QY	2228	TATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCGAGAAAGTCAAAATGCGA	2287
1148	AY	TATTGAATTAATCTTCAATCTTTACCGATGTTGTTAGTGTGAGCAATTTTATTTCGG	1207	Db	2221	TATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCGAGAAAGTCAAAATGCGA	2280
1141	Db	TATTGAATTAATCTTCAATCTTTACCGATGTTGTTAGTGTGAGCAATTTTATTTCGG	1200	QY	2288	AGCGACTCAGTGTAGTACGCGGAATTTTACTTCAAGATCCAAACTTTAGAGGGATCAATAGAC	2347
1208	AY	GAGGACATCAGTAATATCTAGCCTTATAGGAGTGTGTAACAATCTCTCTATATATG	1267	Db	2281	AGCGACTCAGTGTAGTACGCGGAATTTTACTTCAAGATCCAAACTTTAGAGGGATCAATAGAC	2340
1201	Db	GAGGACATCAGTAATATCTAGCCTTATAGGAGTGTGTAACAATCTCTCTATATATG	1260	QY	2348	AACCGACCGTGTGAGAGGAGTACAGATATTACCATCCAAAGGAGGATCAATAGAT	2407
1268	AY	GAAGAGAGCGCAACACGAGAGCTCCAGATCTCTTTTAAATGACCGGTATTAGGA	1327	Db	2341	AACCGACCGTGTGAGAGGAGTACAGATATTACCATCCAAAGGAGGATCAATAGAT	2400
1261	Db	GAAGAGAGCGCAACACGAGAGCTCCAGATCTCTTTTAAATGACCGGTATTAGGA	1320	QY	2408	TCAGAGGAATTTAGTCCACACTACCGGTACCGTTGATGAGTCTATCCAACTGATTTAT	2467
1328	AY	CTTTATCAATCTCTCTTTACGATTTATACAGCACTTGTCCAGCGCCACCACTTTAAT	1387	Db	2401	TCAGAGGAATTTAGTCCACACTACCGGTACCGTTGATGAGTCTATCCAACTGATTTAT	2460
1321	Db	CTTTATCAATCTCTCTTTACGATTTATACAGCACTTGTCCAGCGCCACCACTTTAAT	1380	QY	2468	ATCAGAAATAGATGAGTCCGAATTTAAAGCTTATATCCGTTATGAAATTAAGAGGGTATA	2527
1388	AY	TACGTGTGTGAGGAGTGTAGATTTTCTACACTACCAATAGCTTTTACGTATGACGAA	1447	Db	2461	ATCAGAAATAGATGAGTCCGAATTTAAAGCTTATATCCGTTATGAAATTAAGAGGGTATA	2520
1381	Db	TACGTGTGTGAGGAGTGTAGATTTTCTACACTACCAATAGCTTTTACGTATGACGAA	1440	QY	2528	TCGAGATAGTCAAGCTTGAAGTCTATTTGATCGGTACAAATGCAAAACACGAAATAG	2587
1448	AY	GAGGTACGGTGTGATCTTTTAACTGAAATTTACCGCTGAGGATAATAGTGTGCCACCTCGC	1507	Db	2521	TCGAGATAGTCAAGCTTGAAGTCTATTTGATCGGTACAAATGCAAAACACGAAATAG	2580
1441	Db	GAGGTACGGTGTGATCTTTTAACTGAAATTTACCGCTGAGGATAATAGTGTGCCACCTCGC	1500	QY	2588	TAAATGTGCGAGGCAACGGGTTCTTATGCGCGCTTCAGCCCAAGTCCCAATCGGAAAGT	2647
1508	AY	AAGGATATAGTCTCTTATGTCATGCACTTTTGTTCGAAGATCTGGAACACCTTTT	1567	Db	2581	TAAATGTGCGAGGCAACGGGTTCTTATGCGCGCTTCAGCCCAAGTCCCAATCGGAAAGT	2640
1501	Db	AAGGATATAGTCTCTTATGTCATGCACTTTTGTTCGAAGATCTGGAACACCTTTT	1560	QY	2648	GTGAGAACCGGAATCGATGCGCGCCACACTTTGAAATGGAATCTGATCTAGATTGTCCT	2707
1568	AY	TAAACACTGTGTAGTATTTCTTGAGCGCATCGTAGTCACTCTTACAAATACAAATG	1627	Db	2641	GTGAGAACCGGAATCGATGCGCGCCACACTTTGAAATGGAATCTGATCTAGATTGTCCT	2700
1561	Db	TAAACACTGTGTAGTATTTCTTGAGCGCATCGTAGTCACTCTTACAAATACAAATG	1620	QY	2708	GCAG	2711
1628	AY	ATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGATTTAGAGTTGGGGGGCACT	1687	Db	2701	GCAG	2704
1621	Db	ATCCAGAGAGAAATTAATCAAAATACCTTTAGTGAAGATTTAGAGTTGGGGGGCACT	1680				
1688	AY	CTGTCAATACAGGACAGGATTTACAGAGGGGATATCCCTCGAAGAAATACCTTTGGTG	1747				
1681	Db	CTGTCAATACAGGACAGGATTTACAGAGGGGATATCCCTCGAAGAAATACCTTTGGTG	1740				
1748	AY	ATTTGTATCTCTACAAGTCAATATTAATTCACCAATTTACCCAAAGATACCGTTAAGAT	1807				
1741	Db	ATTTGTATCTCTACAAGTCAATATTAATTCACCAATTTACCCAAAGATACCGTTAAGAT	1800				
1808	AY	TTCGTTAGCTTCCAGTAGGATGAGGATGATGATTTAATTAACAGGAGCGGCATCCACAG	1867				
1801	Db	TTCGTTAGCTTCCAGTAGGATGAGGATGATGATTTAATTAACAGGAGCGGCATCCACAG	1860				
1868	AY	GAGTGGGAGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATAGGGGAGA	1927				
1861	Db	GAGTGGGAGCGCAAGTTAGTGTAGATATGCTCTTCAGAAACTATGGAATAGGGGAGA	1920				
1928	AY	ACTTACATCTAGACATTTAGATATACCGATTTTATGATCTTTTCAATTTAGAGCTA	1987				
1921	Db	ACTTACATCTAGACATTTAGATATACCGATTTTATGATCTTTTCAATTTAGAGCTA	1980				
1988	AY	ATCCAGATATTTGGGTAAGTGAACACCTCTTATTTGGTGAGGCTCTATTATTAGTAGG	2047				
1981	Db	ATCCAGATATTTGGGTAAGTGAACACCTCTTATTTGGTGAGGCTCTATTATTAGTAGG	2040				
2048	AY	TTGAACTTTATATAGATTAATTTGAATTTTCTTAGCAGATGCAACATTTGAGCAGAT	2107				
2041	Db	TTGAACTTTATATAGATTAATTTGAATTTTCTTAGCAGATGCAACATTTGAGCAGAT	2100				
2108	AY	CTGATTTAGAAAGACACAAAGCGGTGAATGCCCTTCTTCTTCTTCCATCAATATCG	2167				
2101	Db	CTGATTTAGAAAGACACAAAGCGGTGAATGCCCTTCTTCTTCTTCCATCAATATCG	2160				
	AY	GGTTAAAAACCGATGTGACGGGATTTATCATATTGATCAGATATCCAAATTTAGTGTGAT	2220				

RESULT 4

AAQ10181

AAQ10181 standard; DNA; 3567 BP.

XX AAQ10181;

XX 25-MAR-2003 (updated)

DT 20-MAR-1991 (first entry)

XX

XX Lepidopteran-active toxin C gene (811B2).

XX Lepidopteran-active toxin C, pest control; as.

KW

XX Bacillus thuringiensis PS81L (NRRL B-18484).

XX EP405810-A.

XX

XX 02-JAN-1991.

PD

XX

XX 18-JUN-1990; 90EP-0306594.

PF

XX

XX 14-DEC-1989; 89US-0451261.

PR

XX

XX 27-JUN-1989; 89US-0371955.

PR

XX

XX (MYCO) MYCOGEN CORP.

PA

XX

XX Payne J, Sick AJ;

PI

XX

XX WPI; 1991-009132/02.

DR

XX

XX P-PSDB; AAR10128.

DR

XX

XX Bacillus thuringiensis contg. DNA encoding lepidopteran-active

PT

XX

XX toxin - use of microorganisms transformed with the toxin gene

PT

RESULT 4

AAQ10181
TD AAQ10181 standard; DNA; 3567 BP.

AC AAQ10181;

XX 25-MAR-2003 (updated)

DT 20-MAR-1991 (first entry)

XX Lepidopteran-active toxin C gene (811B2).

DE Lepidopteran-active toxin C; pest control; as.

XX Bacillus thuringiensis PS81L (NRRL B-18484).

PN EP405810-A.

XX 02-JAN-1991.

XX 18-JUN-1990; 90EP-0306594.

XX 14-DEC-1989; 89US-0451261.

PR 27-JUN-1989; 89US-0371955.

XX (MYCO) MYCOGEN CORP.

XX Payne J, Sick AJ;

DR WPI; 1991-009132/02.

XX P-PSDB; AAR10128.

PT Bacillus thuringiensis contg. DNA encoding lepidopteran-active toxin - use of microorganisms transformed with the toxin gene

PT	in pest control	
XX	Claim 5; Page 19-23; 28pp; English.	
XX	Expression of the toxin gene by a host results, directly or indirectly, in the intracellular prodn. and maintenance of the pesticide.	
CC	See also AQ10179-82.	
CC	(updated on 25-MAR-2003 to correct PA field.)	
XX	Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;	
Query Match	89.7%; Score 2432.6; DB 12; Length 3567;	
Best Local Similarity	95.0%; Pred. No. 0;	
Matches 2447; Conservative	0; Mismatches 24; Indels 0; Gaps 0;	
QY	241 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAAAATGTTTAAAGTAATCTGAAGAA 300	
DB	1 ATGGAGGAAATTAATCAAAATCAATGCATACCTTCAAAATGTTTAAAGTAATCTGAAGAA 60	
QY	301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATGATATTTCTGTCA 360	
DB	61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAAATTAATCAATGATATTTCTGTCA 120	
QY	361 CTGTGTCAGTTCTGTGATCTAACTTTGTACAGGGGGAGGATTTTGTAGTGAATTAATA 420	
DB	121 CTGTGTCAGTTCTGTGATCTAACTTTGTACAGGGGGAGGATTTTGTAGTGAATTAATA 180	
QY	421 GATTTTGTATGGGATAGTTCGCCCTTCTCAATGGGATGCATTTCTAGTACAAATGAA 480	
DB	181 GATTTTGTATGGGATAGTTCGCCCTTCTCAATGGGATGCATTTCTAGTACAAATGAA 240	
QY	481 CAATTAATTAATGAAGAAATAGTGAATTTGCTAGGAATGCTGCTAATTTAGAA 540	
DB	241 CAATTAATTAATGAAGAAATAGTGAATTTGCTAGGAATGCTGCTAATTTAGAA 300	
QY	541 GGAATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGATGGGAAGATCCT 600	
DB	301 GGAATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGATGGGAAGATCCT 360	
QY	601 AATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTTGGTACTTCAATCGGCTACTT 560	
DB	361 AATAATCCAGCAACAGGACAGAGTAATTTGATCGCTTTTGGTACTTCAATCGGCTACTT 420	
QY	661 GAAAGGACATTCCTTCGTTTGGAAATTTCTGGATTTGAAAGTACCCCTTTTATCCGTTTAT 720	
DB	421 GAAAGGACATTCCTTCGTTTGGAAATTTCTGGATTTGAAAGTACCCCTTTTATCCGTTTAT 480	
QY	721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTAAATTTTGGAGAAGA 780	
DB	481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTAAATTTTGGAGAAGA 540	
QY	781 TTGGGATTCACACGATTAATCTCAATGAATACTATATAGACTAATTAAGGATATTGAT 840	
DB	541 TTGGGATTCACACGATTAATCTCAATGAATACTATATAGACTAATTAAGGATATTGAT 600	
QY	841 GAATATGCTGATCACTGTGCAAAATAGTATAATCGGGGATTAATAATTTACCGAAATCT 900	
DB	601 GAATATGCTGATCACTGTGCAAAATAGTATAATCGGGGATTAATAATTTACCGAAATCT 660	
QY	901 ACGTATCAAGATTTGATATATATATCAATTCAGGAGACCTTAACATTTGACTGTATTA 960	
DB	661 ACGTATCAAGATTTGATATATATATCAATTCAGGAGACCTTAACATTTGACTGTATTA 720	
QY	961 GATATCGGCCCTTTCTTTCCAACTATGACATAGGAGATATCCAAATTCAGGCAGTTGGT 1020	
DB	721 GATATCGGCCCTTTCTTTCCAACTATGACATAGGAGATATCCAAATTCAGGCAGTTGGT 780	
QY	1021 CAACTAAACAGGAGATTTATACGGACCCATTAATTTTAAATTCACAGTTACAGTCT 1080	
DB	781 CAACTAAACAGGAGATTTATACGGACCCATTAATTTTAAATTCACAGTTACAGTCT 840	
QY	1081 GTAGCTCAATTACCTATTTTAAACGTTATGGAGACGCGCAATTTAGAAATCCTCATTTA 1140	

DB	841 GTAGCTCAATTACCTACTTTTAAACGTTATGGAGACGCGCAATTTAGAAATCCTCATTTA 900	
QY	1141 TTTGATATATTAATTAATCTTACAAATCTTTACGGAATGGTTTGTAGTGGAGCGCAATTTT 1200	
DB	901 TTTGATATATTAATTAATCTTACAAATCTTTACGGAATGGTTTGTAGTGGAGCGCAATTTT 960	
QY	1201 TATTCGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGGTGGTAACAATACATCTCCT 1260	
DB	961 TATTCGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGGTGGTAACAATACATCTCCT 1020	
QY	1261 ATATATGGAAGAGAGCGGAAACAGAGACCTTCAAGATCTTTACTTTTAAATGGAACCGGTA 1320	
DB	1021 ATATATGGAAGAGAGCGGAAACAGAGACCTTCAAGATCTTTACTTTTAAATGGAACCGGTA 1080	
QY	1321 TTTTGGACCTTTTCAATCTCTACTTTTACGATTTATACGAACCTTTGCCAGCGCCACCA 1380	
DB	1081 TTTTGGACCTTTTCAATCTCTACTTTTACGATTTATACGAACCTTTGCCAGCGCCACCA 1140	
QY	1381 TTTTAAATTTACGTGGTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT 1440	
DB	1141 TTTTAAATTTACGTGGTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTACGTAT 1200	
QY	1441 GCGAAGAGAGTACCGTGTGATTTCTTAACTGAATTAACCGCCTGAGGATTAATAGTGGCCA 1500	
DB	1201 GCGAAGAGAGTACCGTGTGATTTCTTAACTGAATTAACCGCCTGAGGATTAATAGTGGCCA 1260	
QY	1501 CCTCGGAGGATATAGTCATCTGTTTATGTCATGCAACTTTTGTTCGAAGATCTGGAAACA 1560	
DB	1261 CCTCGGAGGATATAGTCATCTGTTTATGTCATGCAACTTTTGTTCGAAGATCTGGAAACA 1320	
QY	1561 CCTTTTAAACAACCTGGTGTAGTATTTTCTTGGAGCGCATCGTAGTGCACACTCTTACAAAT 1620	
DB	1321 CCTTTTAAACAACCTGGTGTAGTATTTTCTTGGAGCGCATCGTAGTGCACACTCTTACAAAT 1380	
QY	1621 ACAATTTGATCCAGAGAGAAATTAATCAATACTTTTGTAGTGAAGAGATTTAGTGGGG 1680	
DB	1381 ACAATTTGATCCAGAGAGAAATTAATCAATACTTTTGTAGTGAAGAGATTTAGTGGGG 1440	
QY	1681 GGCACCTCTGTCATTTACAGGACAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACC 1740	
DB	1441 GGCACCTCTGTCATTTACAGGACAGGATTTACAGGAGGGGATATCCTTCGAAGAAATACC 1500	
QY	1741 TTTTGTGATTTTGTATCTCTCAAGTCAATATTTAATTCACCAATTTACCAAGATACCGT 1800	
DB	1501 TTTTGTGATTTTGTATCTCTCAAGTCAATATTTAATTCACCAATTTACCAAGATACCGT 1560	
QY	1801 TTAAGATTTTGTACGTTTCCAGTAGGGATGACAGGATTTATAGTATTTAACAGGAGCGCA 1860	
DB	1561 TTAAGATTTTGTACGTTTCCAGTAGGGATGACAGGATTTATAGTATTTAACAGGAGCGCA 1620	
QY	1861 TCCACAGAGTGGGAGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAACTATGGAATA 1920	
DB	1621 TCCACAGAGTGGGAGCGCAAGTTAGTGTAGATATGCTCTTTCAGAAACTATGGAATA 1680	
QY	1921 GGGGAGAACTTAAACATCTAGAACATTTAGATATACCGATTTTGTAGTAACTCTTTTCAAT 1980	
DB	1681 GGGGAGAACTTAAACATCTAGAACATTTAGATATACCGATTTTGTAGTAACTCTTTTCAAT 1740	
QY	1981 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACCACTCTATTTTGGTGCAGGTTCTATT 2040	
DB	1741 AGAGCTAATCCAGATATTAATTTGGGATAAGTGAACCACTCTATTTTGGTGCAGGTTCTATT 1800	
QY	2041 AGTAGCGTTGAACCTTTATATAGATAAATTTGAATTTTCTAGCAGATGCAACATTTGAA 2100	
DB	1801 AGTAGCGTTGAACCTTTATATAGATAAATTTGAATTTTCTAGCAGATGCAACATTTGAA 1860	
QY	2101 GCAGAACTCTGATTTAGAAAGAGACAAAGCGGTGAATGCCCTTTTACTTTCTCCAAAT 2160	
DB	1861 GCAGAACTCTGATTTAGAAAGAGACAAAGCGGTGAATGCCCTTTTACTTTCTCCAAAT 1920	
QY	2161 CAAATCGGGTTAAACCGGATGTGCGGATTTATCATTTTGTATCAAGTATCCAAATTTAGTG 2220	

DB 1921 CAAATCGGTTAAACCGATGTGACGGATTAATCAATTAATGATCAATCAATTTAGTG 1980
QY 2221 GATTGTTTATCAGATGAATTTGCTGGATGAAGGAGAGATTTGTCGAGAAATGCAAA 2280
DB 1981 GATTGTTTATCAGATGAATTTGCTGGATGAAGGAGAGATTTGTCGAGAAATGCAAA 2040
QY 2281 CATGCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCAAACTTCAGAGGATC 2340
DB 2041 CATGCGAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCAAACTTCAGAGGATC 2100
QY 2341 AATAGACAACACGACCGTGGCTGGAGAGAGATCAGATATTACCAATCCAAAGGAGAT 2400
DB 2101 AATAGACAACACGACCGTGGCTGGAGAGAGATCAGATATTACCAATCCAAAGGAGAT 2160
QY 2401 GACGTATTCAAGAGAAATACGTCACACTACCGGTACCGTTGATGAGTCTTATCCAAAG 2460
DB 2161 GACGTATTCAAGAGAAATACGTCACACTACCGGTACCGTTGATGAGTCTTATCCAAAG 2220
QY 2461 TATTTATATCAGAAATAGATGAGTCGAAATTAAGGCTTATACCGGTTATGAATTAAGA 2520
DB 2221 TATTTATATCAGAAATAGATGAGTCGAAATTAAGGCTTATACCGGTTATGAATTAAGA 2280
QY 2521 GGTATATCGAAGTAGTCAAGCTTAGAATCTATTTGATCGGTACAAATGCAAAACAC 2580
DB 2281 GGTATATCGAAGTAGTCAAGCTTAGAATCTATTTGATCGGTACAAATGCAAAACAC 2340
QY 2581 GAAATAGTAATGTGCGAGGACCGGTCCTTATGCGGCTTTCAGCCCAAAAGTCCAAATC 2640
DB 2341 GAAATAGTAATGTGCGAGGACCGGTCCTTATGCGGCTTTCAGCCCAAAAGTCCAAATC 2400
QY 2641 GGAAGTGTGGAGAACCGGAATCGATGCGGCGACACCTTGAATCGGATCTGATCTAGAT 2700
DB 2401 GGAAGTGTGGAGAACCGGAATCGATGCGGCGACACCTTGAATCGGATCTGATCTAGAT 2460
QY 2701 TGTTCCTGCAG 2711
DB 2461 TGTTCCTGCAG 2471

RESULT 5
ID AAQ80646 standard; cDNA; 3567 BP.
XX AAQ80646;
XX
DT 25-MAR-2003 (updated)
XX 09-OCT-1995 (first entry)
XX
DE CryIC gene.
XX
KW Crystal protein; toxin; insecticide; ss.
XX
OS Bacillus thuringiensis sub species entomocidus 60.5.
XX
PH Key Location/Qualifiers
FI CDS 1..3567
FI /*tag= a
XX
XX W09506730-A1.
XX
XX 09-MAR-1995.
XX
XX 01-SEP-1994; 94WO-EP02909.
XX
XX 02-SEP-1993; 93GB-0018207.
XX
XX (SANO) SANDOZ LTD.
XX (SANO) SANDOZ PATENT GMBH.
XX (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX Bosch HJ, Stiekema WJ;
XX WPI; 1995-115446/15.
DR

DR P-PSDB; AAR71463.
XX New Bacillus thuringiensis hybrid toxin fragment - derived from
PT two different cry proteins, and related hybrid toxins,
PT recombinant DNA, vectors, transformed plants and microorganisms,
PT for insect control.
XX
XX) Disclosure; Page 18-23; 65pp; English.
XX
CC Crystal proteins CryIC, CryIIE and CryIJA are toxic to lepidopterans.
CC CryIC is particularly active against S. exigua and M. brassicae.
CC Toxic fragments of crystal proteins are thought to be composed of
CC three distinct structural domains. Domain I, the most N-terminal
CC domain, consists of 7 alpha-helices. Domain II comprises 3 beta-
CC sheets and domain III (the most C-terminal) folds into a beta-
CC sandwich. If projected onto CryI sequences, domain I runs from about
CC AA residue 28-260, domain II from about 260-460 and domain III from
CC about 460-600.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 3567 BP; 1168 A; 596 C; 792 G; 1011 T; 0 other;
SQ
Query Match 89.7%; Score 2431; DB 16; Length 3567;
Best Local Similarity 99.0%; Pred. No. 0; Indels 0; Gaps 0;
Matches 2446; Conservative 0; Mismatches 25;
QY 241 ATGGAGGAAAAATCAAAATCAATGATACCTTCAAAATGTTTAAAGTAACTCGAGAA 300
DB 1 ATGGAGGAAAAATCAAAATCAATGATACCTTCAAAATGTTTAAAGTAACTCGAGAA 60
QY 301 GTACTTTTGGATGGAGAACCGGATATCACTGGTAACTCAATTTGATTTCTCTGCA 360
DB 61 GTACTTTTGGATGGAGAACCGGATATCACTGGTAACTCAATTTGATTTCTCTGCA 120
QY 361 CTGTGTCAGTTCTCTGATATCTTAACTTTGTACCGGGGAGGATTTTGTGATTAATA 420
DB 121 CTGTGTCAGTTCTCTGATATCTTAACTTTGTACCGGGGAGGATTTTGTGATTAATA 180
QY 421 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTCAAAATTTGAA 480
DB 181 GATTTTGTATGGGAAATAGTTGGCCCTTCTCAATGGGATGATTTCTAGTCAAAATTTGAA 240
QY 481 CAATTAATTAAGAAAGATAGCTGAATTTGTAGGAATGCTGCTATTCTTAATTTAGAA 540
DB 241 CAATTAATTAAGAAAGATAGCTGAATTTGTAGGAATGCTGCTATTCTTAATTTAGAA 300
QY 541 GGATTTAGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCT 600
DB 301 GGATTTAGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAAATGGGAAGATCCT 360
QY 601 AATATCCAGACACGAGGACGAGATTAATTTGATCGCTTTCGTATCTAGTGGGCTACTT 660
DB 361 AATATCCAGAAACACGAGGACGAGATTAATTTGATCGCTTTCGTATCTAGTGGGCTACTT 420
QY 661 GAAGGGACATTCCTTCGTTTCAATTTCTGGAATTTGGAATGAGTACCCCTTTTATCCGTTTAT 720
DB 421 GAAGGGACATTCCTTCGTTTCAATTTCTGGAATTTGGAATGAGTACCCCTTTTATCCGTTTAT 480
QY 721 GCTCAAGCGGCAATCTGCAATCTAGCTATTAATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCAATCTGCAATCTAGCTATTAATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTGGATTTGACAAACGATTAATGTCATGAATTAATTAAGAGATTTCTGTAATTTTGGAGAAAGA 840
DB 541 TTGGATTTGACAAACGATTAATGTCATGAATTAATTAAGAGATTTCTGTAATTTTGGAGAAAGA 600
QY 841 GAATATGCTGATCACTGTGCAAAATACGATTAATTTGGGATTAATTTTACCGGAATCT 900
DB 601 GAATATGCTGATCACTGTGCAAAATACGATTAATTTGGGATTAATTTTACCGGAATCT 660
QY 901 ACGTATCAAGATTGGATAACATTAATCGATTACGAGAGACTTAAGAGTCTGATTA 960
DB 661 ACGTATCAAGATTGGATAACATTAATCGATTACGAGAGACTTAAGAGTCTGATTA 720

Db 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTGTAGTAATCTCTTTTCAATTT 1740

QY 1981 AGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACCTCTAATTTGGTGCAGGTTCTATT 2040

Db 1741 AGAGCTAAATCCAGATATAATTTGGGATAAGTGAACAACCTCTAATTTGGTGCAGGTTCTATT 1800

QY 2041 AGTAGGTTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 2100

Db 1801 AGTAGGCGGTGAACCTTTATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAA 1860

QY 2101 GCAGAAATCTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTTTACTTCTTCCCAAT 2160

Db 1861 GCAGAAATCTGATTTAGAAAGAGACAAAGGCGGTGAATGCGCTGTTTACTTCTTCCCAAT 1920

QY 2161 CAAATCGGTTAAAAACCGATGTGACGGAATTAATCATATTTGATCAAGTATCCCAATTTAGTG 2220

Db 1921 CAAATCGGTTAAAAACCGATGTGACGGAATTAATCATATTTGATCAAGTATCCCAATTTAGTG 1980

QY 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAGAAATTTGTCGAGAAAGTCAAA 2280

Db 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGGAGAAATTTGTCGAGAAAGTCAAA 2040

QY 2281 CATGCGAAGCGACTCAGTGTGATGAGCGGAATTTTACTTCAAGATCCAACTTCAGAGGGATC 2340

Db 2041 CATGCGAAGCGACTCAGTGTGATGAGCGGAATTTTACTTCAAGATCCAACTTCAGAGGGATC 2100

QY 2341 AATAGACAACACGACCGTGTGAGAGGAAGTACAGATATTACCATCCAAAGGAGAGAT 2400

Db 2101 AATAGACAACACGACCGTGTGAGAGGAAGTACAGATATTACCATCCAAAGGAGAGAT 2160

QY 2401 GAGTATTTCAAGAGAAATTAAGTCACTACCGGGTACCGTTGATGAGTGTCTATCCAAAG 2460

Db 2161 GAGTATTTCAAGAGAAATTAAGTCACTACCGGGTACCGTTGATGAGTGTCTATCCAAAG 2220

QY 2461 TATTTTATACAGAAATAGATGAGTGAATTTAAAGCTTATACCGTTTATGAATTAAGA 2520

Db 2221 TATTTTATACAGAAATAGATGAGTGAATTTAAAGCTTATACCGTTTATGAATTAAGA 2280

QY 2521 GGGTATATCGAAGATAGTCAAGACTTGAATCTATTGATCGGTACATGATGCAAAACAC 2580

Db 2281 GGGTATATCGAAGATAGTCAAGACTTGAATCTATTGATCGGTACATGATGCAAAACAC 2340

QY 2581 GAAATAGTAATGTGCCAGCAGCGGTTCTTATGCGCTTTTACGCCCAAAAGTCCAATC 2640

Db 2341 GAAATAGTAATGTGCCAGCAGCGGTTCTTATGCGCTTTTACGCCCAAAAGTCCAATC 2400

QY 2641 GGAAGTGTGGAAACCGAATCGATGCGGCCACACCTTGAATGGAATCTGATCTAGAT 2700

Db 2401 GGAAGTGTGGAAACCGAATCGATGCGGCCACACCTTGAATGGAATCTGATCTAGAT 2460

QY 2701 TGTTCCTGCAG 2711

Db 2461 TGTTCCTGCAG 2471

RESULT 7

AAV27848

ID AAV27848 standard; DNA; 3567 BP.

XX AC

XX AAV27848;

XX DT

XX 30-SEP-1998 (first entry)

XX DE

XX DNA encoding a mutated CryIC protein designated CryIC.499.

XX KW

KW Mutant; CryIC delta-endotoxin; CryIC.579; insecticidal activity;

KW control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;

KW Trichoplusia ni; Spodoptera frugiperda; ss.

XX OS

OS Synthetic.

XX OS

OS Bacillus thuringiensis.

XX FH

FH Key Location/Qualifiers

CDS

FT FT 1..3567

FT FT /tag= a

FT mutation /note= "no stop codon given"

FT FT 360

FT FT /tag= a

FT mutation /note= "T changed to C"

FT FT 361

FT FT /tag= b

FT FT /note= "A changed to C"

XX WO9823641-Al.

PN 04-JUN-1998.

XX 26-NOV-1997; 97WO-US22181.

XX 27-NOV-1996; 96US-0757536.

XX (ECOG-) ECOGEN INC.

XX Baum JA, Gilmer AJ, Mettuss A;

XX WPI; 1998-322660/28.

XX P-PSDB; AAW61340.

XX New Bacillus thuringiensis nucleic acid segments - comprising

XX delta-endotoxin gene fragments, used for the control of insects,

XX particularly Lepidopteran pests

XX Claim 4; Pages 130-131; 270pp; English.

XX The present sequence encodes a mutant of the CryIC delta-endotoxin

XX of Bacillus thuringiensis designated CryIC.499, where the Asn at

XX position 121 of the wild type CryIC protein is substituted with His.

XX The protein shows insecticidal activity, and can be sprayed onto

XX plants or expressed in transgenic plants for the control of insects,

XX particularly Lepidopteran pests such as Spodoptera exigua, Plutella

XX xylostella, Trichoplusia ni and Spodoptera frugiperda.

XX Sequence 3567 BP; 1167 A; 599 C; 791 G; 1010 T; 0 other;

SQ

Query Match

Best Local Similarity 89.6%; Score 2429.4; DB 19; Length 3567;

Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATAAATCAAAATCAATGCAATCACTTACATTTGTTAAGTAATCTCGAAGAA 300

Db 1 ATGGAGGAAATAAATCAAAATCAATGCAATCACTTACATTTGTTAAGTAATCTCGAAGAA 60

QY 301 GTACTTTTGGATGGAGAACGGATATCACTGCTGAATTAATCAATTTGATATTTCTCTGTCA 360

Db 61 GTACTTTTGGATGGAGAACGGATATCACTGCTGAATTAATCAATTTGATATTTCTCTGTCA 120

QY 361 CTGTTCAGTTTCTGTTATCTAACTTTGTACAGGGGAGGATTTTGTAGTGGATTAATA 420

Db 121 CTGTTCAGTTTCTGTTATCTAACTTTGTACAGGGGAGGATTTTGTAGTGGATTAATA 180

QY 421 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480

Db 181 GATTTTGTATGGGAATAGTTGGCCCTTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240

QY 481 CAATTAATTAATGAAGAATAGTCAATTTGTCTAGGAATGCTGCTATTCTAATTTAGAA 540

Db 241 CAATTAATTAATGAAGAATAGTCAATTTGTCTAGGAATGCTGCTATTCTAATTTAGAA 300

QY 541 GGATAGGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAATGGGAAGATCCT 600

Db 301 GGATAGGAAACAAATTTCAATATATATGTGGAAGCATTTAAAGAATGGGAAGATCCT 360

QY 601 AATAATCCAGCAACCCAGGACCAAGATTAATGATCGCTTTCTGTTATCTTGTATGGGCTACTT 660

Db 361 AATAATCCAGCAACCCAGGACCAAGATTAATGATCGCTTTCTGTTATCTTGTATGGGCTACTT 420

XX 30-SEP-1998 (first entry)
 XX DNA encoding a mutated Cry1C protein designated Cry1C-R148A.
 XX Mutant; Cry1C delta-endotoxin; Cry1C-R148A; insecticidal activity;
 KW control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;
 KW Trichoplusia ni; Spodoptera frugiperda; ss.
 XX Synthetic.
 OS Bacillus thuringiensis.
 OS Location/Qualifiers
 FH 1..3567
 FT /tag= a
 FT /note= "no stop codon given"
 XX W09823641-A1.
 XX
 XX 04-JUN-1998.
 XX 26-NOV-1997; 97WO-US22181.
 XX 27-NOV-1996; 96US-0757536.
 XX (ECOG-) ECOGEN INC.
 XX Baum JA, Gilmer AJ, Mettus A;
 XX WPI: 1998-322660/28.
 XX P-PSDB; AAM61335.
 XX New Bacillus thuringiensis nucleic acid segments - comprising
 PT delta-endotoxin gene fragments, used for the control of insects,
 PT particularly Lepidopteran pests
 XX Claim 4; Pages 126-127; 270pp; English.
 XX The present sequence encodes a mutant of the Cry1C delta-endotoxin
 CC of Bacillus thuringiensis designated Cry1C-R148A. The protein shows
 CC insecticidal activity, and can be sprayed onto plants or expressed in
 CC transgenic plants for the control of insects, particularly Lepidopteran
 CC pests such as Spodoptera exigua, Plutella xylostella, Trichoplusia ni
 CC and Spodoptera frugiperda.
 XX Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;
 SQ

Query Match 89.6%; Score 2429.4; DB 19; Length 3567;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAATGTTTAAAGTAATCCTGAAGAA 300
 DB 1 ATGGAGGAAATAATCAAAATCAATGCATACCTTACAATGTTTAAAGTAATCCTGAAGAA 60
 QY 301 GTCATTTGGATGGAGAACGGATCACTGGTAATTAATCAATGATATTTCTGTGCA 360
 DB 61 GTCATTTGGATGGAGAACGGATCACTGGTAATTAATCAATGATATTTCTGTGCA 120
 QY 361 CTTGTTCACTTCTGGTATCACTTTGACAGGGGAGGATTTTATGTTGGATTAATA 420
 DB 121 CTTGTTCACTTCTGGTATCACTTTGACAGGGGAGGATTTTATGTTGGATTAATA 180
 QY 421 GATTTTGTATGGGAATAGTTCGCCCTTCTCAATGGATGCATTTCTAGTACAAATTCGA 480
 DB 181 GATTTTGTATGGGAATAGTTCGCCCTTCTCAATGGATGCATTTCTAGTACAAATTCGA 240
 QY 481 CAATTAATTAATGAAGAATAGTCAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 540
 DB 241 CAATTAATTAATGAAGAATAGTCAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA 300
 QY 541 GGATTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGATCCT 600

DB 301 GGATTAGGAACAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGATCCT 360
 QY 601 AATAATCCAGCAACCCAGGACCCAGAGTAATATGATCCGCTTTGCTATATCTTGTATGATGGCTACTTT 660
 DB 361 AATAATCCAGCAACCCAGGACCCAGAGTAATATGATCCGCTTTGCTATATCTTGTATGATGGCTACTTT 420
 QY 661 GAAAGGACATTTCTTGGTTCGAAATTTCTGGATTTGAAGTAACTCCCTTTTATCCGTTTAT 720
 DB 421 GAAAGGACATTTCTTGGTTCGAAATTTCTGGATTTGAAGTAACTCCCTTTTATCCGTTTAT 480
 QY 721 GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAGAAGA 780
 DB 481 GCTCAAGCGGCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAGAAGA 540
 QY 781 TTGGGATTTGCAACACGATAAATGCTCAATGAAACTATAATAGACTAATTTAGGCATATTGAT 840
 DB 541 TGGGGATTTGCAACACGATAAATGCTCAATGAAACTATAATAGACTAATTTAGGCATATTGAT 600
 QY 841 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAAATAATTTTACCGAAATCT 900
 DB 601 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAAATAATTTTACCGAAATCT 660
 QY 901 ACGTATCAAGATTGGATAACATATATCGATTACGAGAGACTTAACATTGACTGTATTA 960
 DB 661 ACGTATCAAGATTGGATAACATATATCGATTACGAGAGACTTAACATTGACTGTATTA 720
 QY 961 GATATCGCGCTTTCTTTCCAAACTATGACATAGAGATATCCAAATTCAGCCAGTTGCT 1020
 DB 721 GATATCGCGCTTTCTTTCCAAACTATGACATAGAGATATCCAAATTCAGCCAGTTGCT 780
 QY 1021 CAACTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 1080
 DB 781 CAACTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 840
 QY 1081 GTAGCTCAATTTACCTACTTTTAAAGTTATGAGAGCAGCGCAATTTAGAAATCCTCATTTA 1140
 DB 841 GTAGCTCAATTTACCTACTTTTAAAGTTATGAGAGCAGCGCAATTTAGAAATCCTCATTTA 900
 QY 1141 TTTGATATATTGAATAATCTTACAACTTTTACGGATGCTTTAGTGTGGAGCAATTTT 1200
 DB 901 TTTGATATATTGAATAATCTTACAACTTTTACGGATGCTTTAGTGTGGAGCAATTTT 960
 QY 1201 TATTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGGTGGTAAACATCAATCTCTCT 1260
 DB 961 TATTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGGTGGTAAACATCAATCTCTCT 1020
 QY 1261 ATATATGGAAGAGAGCGCAACAGAGGCTCAAGATCCTTTTAAATGAGACCGGTA 1320
 DB 1021 ATATATGGAAGAGAGCGCAACAGAGGCTCAAGATCCTTTTAAATGAGACCGGTA 1080
 QY 1321 TTTAGGACTTTTATCAATTTCTTACGATTATTACAGCAACCTTGGCCAGGCCACCAT 1380
 DB 1081 TTTAGGACTTTTATCAATTTCTTACGATTATTACAGCAACCTTGGCCAGGCCACCA 1140
 QY 1381 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTAT 1440
 DB 1141 TTTAATTTACGTTGGTGAAGAGTAGAATTTTCTACACCTTACAAATAGCTTTTACGTAT 1200
 QY 1441 CGAGGAAGAGTACGTTGATTTCTTTAACTGAATTAACGCTGAGGATAATAGTGTGCA 1500
 DB 1201 CGAGGAAGAGTACGTTGATTTCTTTAACTGAATTAACGCTGAGGATAATAGTGTGCA 1260
 QY 1501 CCTCGGAAGGATATAGTTCATCGTTTATGTCATCACTTTTGTTCGAAGATCTGGAACA 1560
 DB 1261 CCTCGGAAGGATATAGTTCATCGTTTATGTCATCACTTTTGTTCGAAGATCTGGAACA 1320
 QY 1561 CCTTTTAAACAACTGGTGTAGTATTTTCTTGGAGCACTCGTAGTGCACCTCTTCAAAAT 1620
 DB 1321 CCTTTTAAACAACTGGTGTAGTATTTTCTTGGAGCACTCGTAGTGCACCTCTTCAAAAT 1380
 QY 1621 ACAATTTGATCCAGAGAGAAATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1680
 DB 1381 ACAATTTGATCCAGAGAGAAATTAATCAATACCTTTTGTGAAAGGATTTAGAGTTTGGGG 1440

QY	1681	GGCACCTCTGTCTATTACAGGACAGGATTTACAGAGGGGATATCTCTCGAGAAATACC	1740
DB	1441	GGCACCTCTGTCTATTACAGGACAGGATTTACAGAGGGGATATCTCTCGAGAAATACC	1500
QY	1741	TTTGGTGAATTTGTATCTCTACAAGTCAATATTAATTCACCAATACCAAGATACCT	1800
DB	1501	TTTGGTGAATTTGTATCTCTACAAGTCAATATTAATTCACCAATACCAAGATACCT	1560
QY	1801	TTAAGATTTTCGTTACGCTTCAGTAGGATGACAGGATATAGTATTAACAGAGCGCA	1860
DB	1561	TTAAGATTTTCGTTACGCTTCAGTAGGATGACAGGATATAGTATTAACAGAGCGCA	1620
QY	1861	TCCACAGGATGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAATATCGAAATA	1920
DB	1621	TCCACAGGATGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAATATCGAAATA	1680
QY	1921	GGGGAACCTTAACATCTAGAACATTTAGATATACCGATTTAGTAAATCTTTTCATTT	1980
DB	1681	GGGGAACCTTAACATCTAGAACATTTAGATATACCGATTTAGTAAATCTTTTCATTT	1740
QY	1981	AGACTAATCCAGATTAATTTGGGTAAGTGAACAACTCTATTTCGTCAGGTTCTATT	2040
DB	1741	AGACTAATCCAGATTAATTTGGGTAAGTGAACAACTCTATTTCGTCAGGTTCTATT	1800
QY	2041	AGTAGCGTGAACCTTATATAGATAAATTTGAAATTTCTAGCAGATCAACATTTGAA	2100
DB	1801	AGTAGCGTGAACCTTATATAGATAAATTTGAAATTTCTAGCAGATCAACATTTGAA	1860
QY	2101	GCAGATCTGATTTAGAAAGGACAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAAT	2160
DB	1861	GCAGATCTGATTTAGAAAGGACAAAGGCGGTGAATGCCCTGTTTACTTCTTCCAAT	1920
QY	2161	CAATTCGGGTTAAAAACCGATGTGACGANTATCATATGATCAAGTATCCATTTAGT	2220
DB	1921	CAATTCGGGTTAAAAACCGATGTGACGANTATCATATGATCAAGTATCCATTTAGT	1980
QY	2221	GATGTTTATCAGATCAATTTTGTCTGATGAAAGCGGAAATTTCTCCGAGAGTCAAA	2280
DB	1981	GATGTTTATCAGATCAATTTTGTCTGATGAAAGCGGAAATTTCTCCGAGAGTCAAA	2040
QY	2281	CATGGAAGCGACTCAGTGTGATGAGCGGAATTTACTTCAAGATCCAAATCTCAGAGGATC	2340
DB	2041	CATGGAAGCGACTCAGTGTGATGAGCGGAATTTACTTCAAGATCCAAATCTCAGAGGATC	2100
QY	2341	AATAGACAAACAGACCGTGGCTGGAGAGGAGTACAGATTTACCATCCAGAGGAGAT	2400
DB	2101	AATAGACAAACAGACCGTGGCTGGAGAGGAGTACAGATTTACCATCCAGAGGAGAT	2160
QY	2401	GACGTATTCAGAGAGATTAACGTACACTACCGGTACCGTTGATGATGCTATCCAAAG	2460
DB	2161	GACGTATTCAGAGAGATTAACGTACACTACCGGTACCGTTGATGATGCTATCCAAAG	2220
QY	2461	TATTTATATCAGAAATAGATGAGTGAATTAAGGCTTATACCGGTTATGAATTAAGA	2520
DB	2221	TATTTATATCAGAAATAGATGAGTGAATTAAGGCTTATACCGGTTATGAATTAAGA	2280
QY	2521	GGGTATTCGAGATAGTCAAGACTTTAGAAATCTATTGATCGCGTACAAATGCAAAACAC	2580
DB	2281	GGGTATTCGAGATAGTCAAGACTTTAGAAATCTATTGATCGCGTACAAATGCAAAACAC	2340
QY	2581	GAATATGATTAATGTCGAGGACCGGTTCTTATGCGCGCTTTCAGGCCCAAGTCCAAATC	2640
DB	2341	GAATATGATTAATGTCGAGGACCGGTTCTTATGCGCGCTTTCAGGCCCAAGTCCAAATC	2400
QY	2641	GGAAAGTGTGGAGACCGAATCGATCGCGCCACACCTTGAATGAATCCCTGATCTAGAT	2700
DB	2401	GGAAAGTGTGGAGACCGAATCGATCGCGCCACACCTTGAATGAATCCCTGATCTAGAT	2460
QY	2701	TGTTCTCTGAG	2711
DB	2461	TGTTCTCTGAG	2471

RESULT 9
AX80039 standard; DNA; 3567 BP.
XX
AC AX80039;
XX
DT 12-AUG-1999 (first entry)
XX
DE B. thuringiensis crystal protein CryIC.499 nucleotide sequence.
XX
KW Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;
lepidopteran insect; CryIC; genetic engineering; mutagenesis; mutant;
caterpillar; beetle; mosquito; toxic; modification; ss.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
FN US914318-A.
XX
PD 22-JUN-1999.
XX
PF 26-NOV-1997; 97US-0980071.
XX
PR 26-NOV-1997; 97US-0980071.
PR 27-NOV-1996; 96US-0757536.
XX
PA (ECOG-) ECOGEN INC.
XX
PI Baum JA, Gilmer AJ, Mettius AL;
XX
DR WPI; 1999-370510/31.
DR P-PSDB; AAY17793.
XX
XX New modified delta-endotoxin crystal proteins from Bacillus
thuringiensis are useful in insecticidal compositions
Example 14; Column 108-110; 144pp; English.
XX
XX The present invention describes a new composition comprising an isolated
polypeptide for modified Bacillus thuringiensis crystal proteins (CryIC).
The polypeptide of the composition is insecticidally-active against
Lepidoptera. The composition is toxic to an insect cell and comprised
within an insecticidal formulation can be used as a plant protective
spray which is toxic to caterpillars, beetles and mosquitoes. The
polypeptide of the composition may be used to kill an insect through
ingestion of the composition directly or by ingestion of a plant coated
with the composition or a transgenic plant that expresses the polypeptide
composition. The insecticidal proteins produced by B. thuringiensis are
harmless to plants and other non-targeted organisms but toxic to their
specific target insect. The polypeptides have improved toxicity so a
reduced amount of bioinsecticide per unit area of treated crop can be
used allowing economic and efficient utilization in the field. The
present sequence encodes a modified B. thuringiensis crystal protein.
XX
XX Query Match 89.6%; Score 2429.4; DB 20; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative
QY 241 ATGCGGAAATATCAAAATCAATGATACCTTCAATTTGTTAAAGTAAATCTCGAAGAA 300
DB 1 ATGCGGAAATATCAAAATCAATGATACCTTCAATTTGTTAAAGTAAATCTCGAAGAA 60
QY 301 GTACTTTTGGATGAGACCGGATATCACTGTAATTTACTCAATTTGATTTCTCTGTCA 360
DB 61 GTACTTTTGGATGAGACCGGATATCACTGTAATTTACTCAATTTGATTTCTCTGTCA 120
QY 361 CTGTGTCAGTTTCTGGTATCTAACTTTGACCGGGGAGGATTTTGTAGTTGATTAATA 420
DB 121 CTGTGTCAGTTTCTGGTATCTAACTTTGACCGGGGAGGATTTTGTAGTTGATTAATA 180

Db	2341	GAATAGTAAATGTGCCAGGACGGGTTCTTATGCGCGCTTTCAGGCCAAGTCCATC	2400
Qy	2641	GGAAAGTGTGGAGAACCGAATCGATCGCGGCAACCTTGAAATGGAACTGACTAGAT	2700
Db	2401	GGAAAGTGTGGAGAACCGAATCGATCGCGGCAACCTTGAAATGGAACTGACTAGAT	2460
Qy	2701	TGTTCTCTGCAG	2711
Db	2461	TGTTCTCTGCAG	2471
RESULT 10			
AAX80019			
ID	AAX80019 standard; DNA; 3567 BP.		
AC	AAX80019;		
CC	12-AUG-1999 (first entry)		
DT	B. thuringiensis crystal protein Cry1C-R148A nucleotide sequence.		
XX	Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;		
KW	lepidopteran insect; Cry1C; genetic engineering; mutagenesis; mutant;		
KW	caterpillar; beetle; mosquito; toxic; modification; ss.		
XX	Bacillus thuringiensis.		
OS	Synthetic.		
XX	US5914318-A.		
FN	22-JUN-1999.		
PD	26-NOV-1997; 97US-0980071.		
PF	26-NOV-1997; 97US-0980071.		
PR	27-NOV-1996; 96US-0757536.		
XX	(ECOG-) ECOGEN INC.		
PA	Baum JA, Gilmer AJ, Mettuss AL;		
PI	WPI; 1999-370510/31.		
DR	P-PSDB; AAY17788.		
XX	New modified delta-endotoxin crystal proteins from Bacillus		
PT	thuringiensis are useful in insecticidal compositions		
PT	Example 5; Column 97-99; 144pp; English.		
XX	The present invention describes a new composition comprising an isolated		
PS	polypeptide for modified Bacillus thuringiensis crystal proteins (Cry1C).		
CC	The polypeptide of the composition is insecticidally-active against		
CC	Lepidoptera. The composition is toxic to an insect cell and comprised		
CC	within an insecticidal formulation can be used as a plant protective		
CC	spray which is toxic to caterpillars, beetles and mosquitoes. The		
CC	polypeptide of the composition may be used to kill an insect through		
CC	ingestion of the composition directly or by ingestion of a plant coated		
CC	with the composition or a transgenic plant that expresses the polypeptide		
CC	composition. The insecticidal proteins produced by B. thuringiensis are		
CC	harmless to plants and other non-targeted organisms but toxic to their		
CC	specific target insect. The polypeptides have improved toxicity so a		
CC	reduced amount of bioinsecticide per unit area of treated crop can be		
CC	used allowing economic and efficient utilization in the field. The		
CC	present sequence encodes a modified B. thuringiensis crystal protein.		
XX	Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;		
SQ			
Query Match 89.6%; Score 2429.4; DB 20; Length 3567;			
Best Local Similarity 98.9%; Pred. No. 0;			
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;			
Qy	241	ATGAGAGAAATCAAAATCAATGCTACCTTACATTTGTTTAAAGTAACTCTGAGAA	300

QY 1381 TTTAATTTAGTGGTGAAGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTAT 1440
 DB |||||
 QY 1441 TTTAATTTAGTGGTGTGAAGAGTAGAATTTTCTACACCTACAAATAGCTTTACGTAT 1200
 DB |||||
 QY 1441 GCAGGAAGAGTACGGTTGATTTCTTAACTGAATTAACCGCTCAGGATTAATAGTGTGCCA 1500
 DB |||||
 QY 1201 CGAGGAAGAGTACGGTTGATTTCTTAACTGAATTAACCGCTCAGGATTAATAGTGTGCCA 1260
 DB |||||
 QY 1501 CCTCGGAAGGATATAGTCAATCGTTTATGTCAATCACTTTTCTTCAAGATCTGGAACA 1560
 DB |||||
 QY 1261 CCTCGGAAGGATATAGTCAATCGTTTATGTCAATCACTTTTCTTCAAGATCTGGAACA 1320
 DB |||||
 QY 1561 CTTTTTTTAACTGGTGTAGTATTTTCTTGACGCAATCGTAGTGCACCTTTTCAAAAT 1620
 DB |||||
 QY 1321 CTTTTTTTAACTGGTGTAGTATTTTCTTGACGCAATCGTAGTGCACCTTTTCAAAAT 1380
 DB |||||
 QY 1621 ACAATTTGATCCAGAGAGATTAATCAATACTTTTGTAGTGAAGAGATTTAGTGTGGGG 1680
 DB |||||
 QY 1381 ACAATTTGATCCAGAGAGATTTAATCAATACTTTTGTAGTGAAGAGATTTAGTGTGGGG 1440
 DB |||||
 QY 1681 GGCACCTCTGTCTATACAGGACAGGATTTACAGGAGGGGATATCTTTCGAAGAAATACC 1740
 DB |||||
 QY 1441 GGCACCTCTGTCTATACAGGACAGGATTTACAGGAGGGGATATCTTTCGAAGAAATACC 1500
 DB |||||
 QY 1741 TTTGGTGAATTTGTATCTCTCAAGTCAATTAATTAATTCACCAATTAACCCAAAGATACCGT 1800
 DB |||||
 QY 1501 TTTGGTGAATTTGTATCTCTCAAGTCAATTAATTAATTCACCAATTAACCCAAAGATACCGT 1560
 DB |||||
 QY 1801 TTAAGATTTTGTACCTTCCAGTAGGATGACAGTATATAGTATTAACAGAGCGGCA 1860
 DB |||||
 QY 1561 TTAAGATTTTGTACCTTCCAGTAGGATGACAGTATATAGTATTAACAGAGCGGCA 1620
 DB |||||
 QY 1861 TCCACAGGAGTGGGAGCCAAAGTTAGTGTAGATATGCTCTTCAGAAAATTAAGAAATA 1920
 DB |||||
 QY 1621 TCCACAGGAGTGGGAGCCAAAGTTAGTGTAAATATGCTCTTCAGAAAATTAAGAAATA 1680
 DB |||||
 QY 1921 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAATCTTTTTCATTT 1980
 DB |||||
 QY 1681 GGGGAGAACTTAACATCTAGAACATTTAGATATACCGATTTTAGTAATCTTTTTCATTT 1740
 DB |||||
 QY 1981 AGAGCTAATCCAGATATATTTGGGTAAGTGAACACCTCTATTGGTCAGGTTCTATT 2040
 DB |||||
 QY 1741 AGAGCTAATCCAGATATATTTGGGTAAGTGAACACCTCTATTGGTCAGGTTCTATT 1800
 DB |||||
 QY 2041 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAATTTATCTAGCAGATCAACATTTGAA 2100
 DB |||||
 QY 1801 AGTAGCGTTGAACCTTTATATAGATAAAATTTGAATTTATCTAGCAGATCAACATTTGAA 1860
 DB |||||
 QY 2101 GCAGAACTGATTTAGAAAGAGCACAAAGCGGGTGAATGCCCTGTTTACTTTCTTCCAAT 2160
 DB |||||
 QY 1861 GCAGAACTGATTTAGAAAGAGCACAAAGCGGGTGAATGCCCTGTTTACTTTCTTCCAAT 1920
 DB |||||
 QY 2161 CAATCGGTTAAAAACCGATGTGACGGATATCATATTTGATCAAGTATCCAAATTTAGTG 2220
 DB |||||
 QY 1921 CAATCGGTTAAAAACCGATGTGACGGATATCATATTTGATCAAGTATCCAAATTTAGTG 1980
 DB |||||
 QY 2221 GATTGTTTATCAGATCAATTTTGTCTGGATGAAAGCGGAGAAATTTGCCGAGAAAGTCAAA 2280
 DB |||||
 QY 1981 GATTGTTTATCAGATCAATTTTGTCTGGATGAAAGCGGAGAAATTTGCCGAGAAAGTCAAA 2040
 DB |||||
 QY 2281 CATCGGAAGCGACTCAGTGTATGAGCGGAATTTTCTTCAAGATCCAACTTCAGAGGGATC 2340
 DB |||||
 QY 2041 CATCGGAAGCGACTCAGTGTATGAGCGGAATTTTCTTCAAGATCCAACTTCAGAGGGATC 2100
 DB |||||
 QY 2341 AATAGACACACCGACCGTGGTGGAGAGAGTACAGATATTAACATCCAAAGAGAGAT 2400
 DB |||||
 QY 2101 AATAGACACACCGACCGTGGTGGAGAGAGTACAGATATTAACATCCAAAGAGAGAT 2160
 DB |||||
 QY 2401 GAGGTATTCAAAGAGAAATTTACGTACACTACCGGGTACCGTTGATGAGTGCTATCCACG 2460
 DB |||||
 QY 2161 GAGGTATTCAAAGAGAAATTTACGTACACTACCGGGTACCGTTGATGAGTGCTATCCACG 2220
 DB |||||

QY 2461 TATTTATATCAGAAATAGATGAGTCGAAATTAAGCTTATATACCGTTTATGAATTAAGA 2520
 DB |||||
 QY 2221 TATTTATATCAGAAATAGATGAGTCGAAATTAAGCTTATATACCGTTTATGAATTAAGA 2280
 DB |||||
 QY 2521 GGGTATATCGAAGATAGTCAAGACTTAGAATCTATTTGATCGCGTACAAATCGAAACAC 2580
 DB |||||
 QY 2281 GGGTATATCGAAGATAGTCAAGACTTAGAATCTATTTGATCGCGTACAAATCGAAACAC 2340
 DB |||||
 QY 2581 GAAATAGTAAATGTGTCAGGACCGGTTCTTATGCGCGCTTTCAGCCCAAAAGTCCAATC 2640
 DB |||||
 QY 2341 GAAATAGTAAATGTGTCAGGACCGGTTCTTATGCGCGCTTTCAGCCCAAAAGTCCAATC 2400
 DB |||||
 QY 2641 GGAAGTGTGGAACCCGAATCGATGCGCGCACACCTTGAATGGAATCCTGATCTAGAT 2700
 DB |||||
 QY 2401 GGAAGTGTGGAACCCGAATCGATGCGCGCACACCTTGAATGGAATCCTGATCTAGAT 2460
 DB |||||
 QY 2701 TGTTCCTGCAG 2711
 DB |||||
 QY 2461 TGTTCCTGCAG 2471
 DB |||||
 RESULT 11
 AAA08144
 ID AAA08144 standard; DNA; 3567 BP.
 XX
 AC AAA08144;
 XX
 DT 27-JUN-2000 (first entry)
 XX
 DE Bacillus thuringiensis CryIC-R148A gene SEQ ID NO:1.
 XX
 KW Bacillus thuringiensis; CryIC; crystal protein; insecticide; insect;
 KW delta-endotoxin; lepidopteran; modification; genetic engineering;
 KW resistance; mutant; mutagenesis; ss.
 XX
 OS Bacillus thuringiensis.
 OS Synthetic.
 XX
 PN US6033874-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 18-MAY-1999; 99US-0314093.
 XX
 PR 26-NOV-1997; 97US-0980071.
 PR 27-NOV-1996; 96US-0757536.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 PI Mettus AL, Baum JA, Gilmer AJ;
 XX
 DR WPI: 2000-255697/22.
 DR P-PSDB; AAY82396.
 XX
 PT New mutant Bacillus thuringiensis endotoxin, used for controlling
 PT lepidopteran pests, has mutated loop region to impart higher
 PT insecticidal activity -
 XX
 PS Example 14; Column 107-110; 153pp; English.
 XX
 CC The present invention describes isolated Bacillus thuringiensis CryIC
 CC delta-endotoxin polypeptides having: (i) at least one amino acid (aa)
 CC mutation in the loop region between alpha-helices 6 and 7 of domain 1;
 CC and (ii) better activity against Lepidoptera than the native CryIC.
 CC The polypeptides, possibly after activation in the digestive tract of
 CC insects, kills insect cells by formation of pores and disturbing
 CC cellular homeostasis. The polypeptides are used to control lepidopteran
 CC pests on plants, either: (i) applied as a composition; or (ii) expressed
 CC in plants from heterologous nucleic acid (generating insect-resistant
 CC plants). They are more active against lepidoptera than native CryIC.
 CC AAA08144 to AAA08182, and AAY82396 to AAY82432, represent sequences used
 CC in the exemplification of the present invention.
 XX

Seq	Sequence	3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;
Qy	Query Match	89.6%; Score 2429.4; DB 21; Length 3567;
Db	Best Local Similarity	98.9%; Pred. No. 0;
Qy	Matches 2445; Conservative	0; Mismatches 26; Indels 0; Gaps 0;
Qy	241	ATGGAGGAAATAATCAAAATCAATGCATACCTTCAATTTGTTTAAGTAATCTCGAAGAA 300
Db	1	ATGGAGGAAATAATCAAAATCAATGCATACCTTCAATTTGTTTAAGTAATCTCGAAGAA 60
Qy	301	GTACTTTTGGATGAGACCGGATCAACTGGTAAATTAATCTCAATTTGATATTTCTCTGCA 360
Db	61	GTACTTTTGGATGAGACCGGATCAACTGGTAAATTAATCTCAATTTGATATTTCTCTGCA 120
Qy	361	CTTGTTGAGTTCTGGTATCTAATCTTTGTACACGGGGGAGGATTTTGTGTTGATTAATA 420
Db	121	CTTGTTGAGTTCTGGTATCTAATCTTTGTACACGGGGGAGGATTTTGTGTTGATTAATA 180
Qy	421	GATTTTGTATGGGATATGTCGGCCCTCTCAATGGGATGCATTTCTAGTACAAATTTGAA 480
Db	181	GATTTTGTATGGGATATGTCGGCCCTCTCAATGGGATGCATTTCTAGTACAAATTTGAA 240
Qy	481	CAATTAATTAATGAAGAATAGTCGATTTGCTTAGGAATGCTGCTATGCTAATTTAGAA 540
Db	241	CAATTAATTAATGAAGAATAGTCGATTTGCTTAGGAATGCTGCTAATTTAGTAATTTAGAA 300
Qy	541	GGATTAGGAAACAATTTCAATATAATGTGGAAGCATTTTAAGAATCGGAGAGATCCT 600
Db	301	GGATTAGGAAACAATTTCAATATAATGTGGAAGCATTTTAAGAATCGGAGAGATCCT 360
Qy	601	AATAATTCAGCAACAACAGGACACAGAGTAATTCATCGCTTTTCGTATCTTGATGGCTACTT 660
Db	361	AATAATTCAGCAACAACAGGACACAGAGTAATTCATCGCTTTTCGTATCTTGATGGCTACTT 420
Qy	661	GAAAGGACATTTCTTGGTTTTCGAAATTTCTCGAATTTGAAGTACCCCTTTTATCCGTTTAT 720
Db	421	GAAAGGACATTTCTTGGTTTTCGAAATTTCTCGAATTTGAAGTACCCCTTTTATCCGTTTAT 480
Qy	721	CTCAGAGCGGCAATCTGCAATCTAGCTATATTAAGAGATCTGTAAATTTTGAGAAAGA 780
Db	481	CTCAGAGCGGCAATCTGCAATCTAGCTATATTAAGAGATCTGTAAATTTTGAGAAAGA 540
Qy	781	TTGGGATTCGAACGATAAATGTCAATGAACATATAATAGACTAATTAGGCATATTTGAT 840
Db	541	TTGGGATTCGAACGATAAATGTCAATGAACATATAATAGACTAATTAGGCATATTTGAT 600
Qy	841	GAATATCTGATCATCTGTGCAATAGCTATATCGGGATTAATAATTTTACCGAAATCT 900
Db	601	GAATATCTGATCATCTGTGCAATAGCTATATCGGGATTAATAATTTTACCGAAATCT 660
Qy	901	ACGTATCAAGATTCGATTAACATATAATTCGATTCGGAGAGATTAACATGACCTGATTA 960
Db	661	ACGTATCAAGATTCGATTAACATATAATTCGATTCGGAGAGATTAACATGACCTGATTA 720
Qy	961	GATATCGCCCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCGAGTTGCT 1020
Db	721	GATATCGCCCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCGAGTTGCT 780
Qy	1021	CAACTTAACAAAGGAGAGTTTATACGGACCAATTAATTTTAAATTTTAAATCCAGTTACAGTCT 1080
Db	781	CAACTTAACAAAGGAGAGTTTATACGGACCAATTAATTTTAAATTTTAAATCCAGTTACAGTCT 840
Qy	1081	GTAGCTCAATTTACTACTTTTAAAGTTATGGAGAGCGCAATTTAGAAATCTCTCATTTA 1140
Db	841	GTAGCTCAATTTACTACTTTTAAAGTTATGGAGAGCGCAATTTAGAAATCTCTCATTTA 900
Qy	1141	TTTGATATTTGATTAATCTTACATCTTTTACGATTTGGTTTGTGTTAGTGTTCGACGCAATTTT 1200
Db	901	TTTGATATTTGATTAATCTTACATCTTTTACGATTTGGTTTGTGTTAGTGTTCGACGCAATTTT 960
Qy	1201	TATTTGGGAGCAATCGATTAATCTAGCTTTATAGAGGTTGTTAACAATACATCTCTCT 1260
Db	961	TATTTGGGAGCAATCGATTAATCTAGCTTTATAGAGGTTGTTAACAATACATCTCTCT 1020

QY 2341 AATAGACAACACGACCGTGGCTGGAGAGGAGTACAGATATTAACCATCCAGGAGGAGAT 2400
 Db AATAGACAACACGACCGTGGCTGGAGAGGAGTACAGATATTAACCATCCAGGAGGAGAT 2160
 QY 2401 GACGTATTTCAAGAGAAATACGTACACTACCGGGTACCGTTGATGAGTCTATCCAAAG 2460
 Db GACGTATTTCAAGAGAAATACGTACACTACCGGGTACCGTTGATGAGTCTATCCAAAG 2220
 QY 2461 TATTTATATCAGAAAATAGATGAGTCAAAATTAAGCTTATACCCGTTATGAATTAAGA 2520
 Db TATTTATATCAGAAAATAGATGAGTCAAAATTAAGCTTATACCCGTTATGAATTAAGA 2280
 QY 2521 GGGTATATCAGATAGTCAAGACTTAGAATCTATTGATCCGTCACATCCAAACAC 2580
 Db GGGTATATCAGATAGTCAAGACTTAGAATCTATTGATCCGTTACAAATCCAAACAC 2340
 QY 2581 GAAATAGTAAATGTCCAGGACCGGTTCCTTATGCGCGCTTTTCAGCCCAAGCTCCAAATC 2640
 Db GAAATAGTAAATGTCCAGGACCGGTTCCTTATGCGCGCTTTTCAGCCCAAGCTCCAAATC 2400
 QY 2641 GGAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2700
 Db GGAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2460
 QY 2701 TGTTCCTGCAG 2711
 Db TGTTCCTGCAG 2471

RESULT 12

AAA08149
 ID AAA08149 standard; DNA; 3567 BP.
 AC AAA08149;
 XX
 DT 27-JUN-2000 (first entry)
 XX
 DE Bacillus thuringiensis CryIC.499 gene SEQ ID NO:11.
 XX
 KW Bacillus thuringiensis; CryIC; crystal protein; insecticide; insect;
 KW delta-endotoxin; lepidopteran; modification; genetic engineering;
 KW resistance; mutant; mutagenesis; sb.
 XX
 OS Bacillus thuringiensis.
 OS Synthetic.
 XX
 PN US6033874-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 18-MAY-1999; 99US-0314093.
 XX
 PR 26-NOV-1997; 97US-0980071.
 PR 27-NOV-1996; 96US-0757536.
 XX
 PA (ECOG-) ECOGEN INC.
 XX
 PI Mettuss AL, Baum JA, Gilmer AJ;
 XX
 DR WPI; 2000-255697/22.
 DR P-PSDB; AAY82401.
 XX
 PT New mutant Bacillus thuringiensis endotoxin, used for controlling
 PT lepidopteran pests, has mutated loop region to impart higher
 PT insecticidal activity -
 XX
 PS Example 14; Column 119-122; 153pp; English.

XX
 CC The present invention describes isolated Bacillus thuringiensis CryIC
 CC delta-endotoxin polypeptides having: (i) at least one amino acid (aa)
 CC mutation in the loop region between alpha-helices 6 and 7 of domain 1;
 CC and (ii) better activity against lepidoptera than the native CryIC.
 CC The polypeptides, possibly after activation in the digestive tract of

CC insects, kills insect cells by formation of pores and disturbing
 CC cellular homeostasis. The polypeptides are used to control lepidopteran
 CC pests on plants, either: (i) applied as a composition; or (ii) expressed
 CC in plants from heterologous nucleic acid (generating insect-resistant
 CC plants). They are more active against lepidoptera than native CryIC.
 CC AAA08144 to AAA08182, and AAY82396 to AAY82432, represent sequences used
 CC in the exemplification of the present invention.

XX
 SQ Sequence 3567 BP; 1167 A; 599 C; 791 G; 1010 T; 0 other;

Query Match 89.6%; Score 2429.4; DB 21; Length 3567;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 QY 241 ATGGAGGAAAATAATCAAAATCAATGTCATACCTTCAAAATGTTTAAAGTAAATCTCGAAGAA 300
 Db 1 ATGGAGGAAAATAATCAAAATCAATGTCATACCTTCAAAATGTTTAAAGTAAATCTCGAAGAA 60
 QY 301 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATTCATCAATGATATTTCTCTGTCA 360
 Db 61 GTACTTTTGGATGGAGAACGGATATCAACTGGTAATTCATCAATGATATTTCTCTGTCA 120
 QY 361 CTTGTTTCAGTTTCTGGTATCTAACTTTGTACACGGGGGAGGATTTTACTTGGATTAATA 420
 Db 121 CTTGTTTCAGTTTCTGGTATCTAACTTTGTACACGGGGGAGGATTTTACTTGGATTAATA 180
 QY 421 GATTTTGTATGGGGAATAGTTCGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTGAA 480
 Db 181 GATTTTGTATGGGGAATAGTTCGCCCTTCTCAATGGGATGCATTTCTAGTACAAATTGAA 240
 QY 481 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTTCTAATTTAGAA 540
 Db 241 CAATTAATTAATGAAGAATAGCTGAATTTGCTAGGAATGCTGCTATTTCTAATTTAGAA 300
 QY 541 GGAATAGGAAACAATTTCAATATATATGTGGAGCAATTTAAAGAATGGGAAGAGATCCT 600
 Db 301 GGAATAGGAAACAATTTCAATATATATGTGGAGCAATTTAAAGAATGGGAAGAGATCCT 360
 QY 601 AATAATCCAGCAACACGAGGACAGAGTAATTTGATCGCTTTCGTATATCTTCAATGGCTACT 660
 Db 361 CATATCCAGCAACACGAGGACAGAGTAATTTGATCGCTTTCGTATATCTTCAATGGCTACT 420
 QY 661 GAAAGGACATTCCTTCGTTTCGAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 720
 Db 421 GAAAGGACATTCCTTCGTTTCGAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTAT 480
 QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTAAATTTTGGAGAAAGA 780
 Db 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTAAATTTTGGAGAAAGA 540
 QY 781 TTGGGATTTGACAAACGATAAATGCTCAATGAAAATTAATAGACTAATTAGGCATATTTGAT 840
 Db 541 TTGGGATTTGACAAACGATAAATGCTCAATGAAAATTAATAGACTAATTAGGCATATTTGAT 600
 QY 841 GAATATGCTGATCACTGTGCAAAATACGTATATTCGGGATTAATAATTTACCGAAATCT 900
 Db 601 GAATATGCTGATCACTGTGCAAAATACGTATATTCGGGATTAATAATTTACCGAAATCT 660
 QY 901 ACGTATCAAGATTTGGATTAACATATATTCGATTCAGGAGAGACTTAACATTTGATTTA 960
 Db 661 ACGTATCAAGATTTGGATTAACATATATTCGATTCAGGAGAGACTTAACATTTGATTTA 720
 QY 961 GATATCGCGCTTCTTTCCAACTATGCAATAGGAGATATCCAAATTCAGCAGCTTGGT 1020
 Db 721 GATATCGCGCTTCTTTCCAACTATGCAATAGGAGATATCCAAATTCAGCAGCTTGGT 780
 QY 1021 CAACCTAAACAGGGAAGTTTATACGGACCAATTAATTTTAAATTCACAGTTTACAGTCT 1080
 Db 781 CAACCTAAACAGGGAAGTTTATACGGACCAATTAATTTTAAATTCACAGTTTACAGTCT 840
 QY 1081 GTAGCTCAATTTACCTACTTTTAACTGTTATGGAGAGACGCGCAATTTAGAAATCCTCATTTA 1140
 Db 841 GTAGCTCAATTTACCTACTTTTAACTGTTATGGAGAGACGCGCAATTTAGAAATCCTCATTTA 900

QY	1141	TTTGATATATGAAATATCTTACAACTTTACGGATTGGTTAGTTGGAGCAATTTT	1200	QY	2221	GATCTTTATCAGATCAATTTTGTCTGGATGAAAGCGGAGAAATTTGTCGGAAGATCAAA	2280
DB	901	TTTGATATATGAAATATCTTACAACTTTACGGATTGGTTAGTTGGAGCAATTTT	960	DB	1981	GATCTTTATCAGATCAATTTTGTCTGGATGAAAGCGGAGAAATTTGTCGGAAGATCAAA	2040
QY	1201	TATTTGGGAGGACATCAGTAAATCTTACAACTTTACGGATTGGTTAGTTGGAGCAATTTT	1260	QY	2281	CATCGAAGGAGCTCAGTGTATGAGCGGAATTTTCTTCAAGATCCAAATTTTCAAGGGATC	2340
DB	961	TATTTGGGAGGACATCAGTAAATCTTACAACTTTACGGATTGGTTAGTTGGAGCAATTTT	1020	DB	2041	CATCGAAGGAGCTCAGTGTATGAGCGGAATTTTCTTCAAGATCCAAATTTTCAAGGGATC	2100
QY	1261	ATATATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTT	1320	QY	2341	ATATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTTCAAGGGATC	2400
DB	1021	ATATATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTT	1080	DB	2101	ATATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTTCAAGGGATC	2160
QY	1321	TTTATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTT	1380	QY	2401	GAGCTTTTCAAGAGAGATTTACCTCACACTACCGGTACCGTTGATGAGTGTATCCAAAGC	2460
DB	1081	TTTATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTT	1140	DB	2161	GAGCTTTTCAAGAGAGATTTACCTCACACTACCGGTACCGTTGATGAGTGTATCCAAAGC	2220
QY	1381	TTTATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTT	1440	QY	2461	TATTTATATCAAGAAATAGATGAGTTCGAATTAAGCTTATACCGTTTATGAATTAAGA	2520
DB	1141	TTTATGAGAGAGGAGCAACAGAGAGCTCCAAAGATCTTTTCTTCAAGATCCAAATTTT	1200	DB	2221	TATTTATATCAAGAAATAGATGAGTTCGAATTAAGCTTATACCGTTTATGAATTAAGA	2280
QY	1441	GCAGAGAGAGGATACGTTGATCTTTAACTGAAATTTACCGCTGAGGATTAATAGTGTGCA	1500	QY	2521	GGTATATCGAAGATAGTCAAGACTTAGAATCTTATGATCGCTCAATGCAAAACAC	2580
DB	1201	GCAGAGAGAGGATACGTTGATCTTTAACTGAAATTTACCGCTGAGGATTAATAGTGTGCA	1260	DB	2281	GGTATATCGAAGATAGTCAAGACTTAGAATCTTATGATCGCTCAATGCAAAACAC	2340
QY	1501	CCTCGGAGAGATATAGTCACTGTTTATGTCAGCACTTTTGTTCAGAGATCTGGAACA	1560	QY	2581	GAAATAGTAAATGTGCCAGGACGCGTTCCTTATGCGCGCTTTCAGCCCAAGTCCCAATC	2640
DB	1261	CCTCGGAGAGATATAGTCACTGTTTATGTCAGCACTTTTGTTCAGAGATCTGGAACA	1320	DB	2341	GAAATAGTAAATGTGCCAGGACGCGTTCCTTATGCGCGCTTTCAGCCCAAGTCCCAATC	2400
QY	1561	CCTTTTAACTGCTGTAGTATTTCTTGTGAGCGCATCGTGTGCACTTTTCAAGATCTGGAACA	1620	QY	2641	GAAAGTGTGGAGAACCGAATCGATGCGCGCACACCTTGATGGAATCCTGATCTAGAT	2700
DB	1321	CCTTTTAACTGCTGTAGTATTTCTTGTGAGCGCATCGTGTGCACTTTTCAAGATCTGGAACA	1380	DB	2401	GAAAGTGTGGAGAACCGAATCGATGCGCGCACACCTTGATGGAATCCTGATCTAGAT	2460
QY	1621	ACAAATGATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGTTGGGGG	1680	QY	2701	TGTTCTCTGCAG 2711	
DB	1381	ACAAATGATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGAGATTTAGTTGGGGG	1440	DB	2461	TGTTCTCTGCAG 2471	
QY	1741	GGCAGCTGTCTTACAGAGCAGGATTTACAGGAGGAGATTCCTTCGAAGAAATACC	1740	DB			
DB	1441	GGCAGCTGTCTTACAGAGCAGGATTTACAGGAGGAGATTCCTTCGAAGAAATACC	1500	DB			
QY	1741	TTTGGTGAATTTGTATCTCTACAGTCAATTAATTTACCAATTTACCAAGATACCGT	1800	DB			
DB	1501	TTTGGTGAATTTGTATCTCTACAGTCAATTAATTTACCAATTTACCAAGATACCGT	1560	DB			
QY	1801	TTAAGATTTCTGTACGCTTCCAGTAGGATGACAGGATTAATGATTAATTAACAGAGCGCA	1860	DB			
DB	1561	TTAAGATTTCTGTACGCTTCCAGTAGGATGACAGGATTAATGATTAATTAACAGAGCGCA	1620	DB			
QY	1861	TCCAGAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAATCTATGGAATA	1920	DB			
DB	1621	TCCAGAGAGTGGGAGGCGCAAGTTAGTGTAGATATGCTCTTCAGAAATCTATGGAATA	1680	DB			
QY	1921	GGGAGAGCTTACATCTAGAACATTTAGATATACCGATTTAGTAATCTTTTTCATTT	1980	DB			
DB	1681	GGGAGAGCTTACATCTAGAACATTTAGATATACCGATTTAGTAATCTTTTTCATTT	1740	DB			
QY	1981	AGAGCTAATCCAGATATATTTGGATAGTGAACCACTCTTATTTGGTGCAGGTTCTATT	2040	DB			
DB	1741	AGAGCTAATCCAGATATATTTGGATAGTGAACCACTCTTATTTGGTGCAGGTTCTATT	1800	DB			
QY	2041	AGTAGCGTTGAATTTATATAGATAAATTTGAATTTTCTAGCAGATCAACATTTGA	2100	DB			
DB	1801	AGTAGCGTTGAATTTATATAGATAAATTTGAATTTTCTAGCAGATCAACATTTGA	1860	DB			
QY	2101	GCAGATCTGATTTTGAAGAGACAAAGGCGGTGAATGCTCTTCTTCTTCTTCAAT	2160	DB			
DB	1861	GCAGATCTGATTTTGAAGAGACAAAGGCGGTGAATGCTCTTCTTCTTCTTCAAT	1920	DB			
QY	2161	CAATCGGGTAAAAACCGATGTGAGCGAATTAATTAATGATCAAGTCCGAATTTAGTG	2220	DB			
DB	1921	CAATCGGGTAAAAACCGATGTGAGCGAATTAATTAATGATCAAGTCCGAATTTAGTG	1980	DB			

RESULT 13

AAD44210

1D AAD44210 standard; DNA; 3567 BP.

AC AAD44210;

XX AAD44210;

DT 13-DEC-2002 (first entry)

XX Bacillus thuringiensis Cry1C-R148A mutant protein encoding DNA.

DE Cry1 protein; delta-endotoxin; insect resistance; lepidopteran insect;

KW transgenic plant; transgenic; mutant; gene; ds.

XX Bacillus thuringiensis.

OS Synthetic.

XX Key Location/Qualifiers

FT 1..3567

CDS /*tag= a

FT /product= "CRY1C-R148A mutant protein"

FT /note= "No stop codon"

FT /partial

XX US6313378-B1;

XX 06-NOV-2001.

XX 21-JUN-1999; 99US-0337635.

XX 26-NOV-1997; 97US-0980071.

XX 27-NOV-1996; 96US-0757536.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Baum JA, Gilmer AJ, Mettus AL;

XX

DR WPI; 2002-033341/04.
DR P-PSDB; ARE26460.
XX Transgenic plants, comprises nucleic acid encoding CryIC
PT delta-endotoxin polypeptide, has improved resistance to Lepidopteran
PT insects
XX
XX Example 5; Column 131-140; 151pp; English.
XX The present invention relates to novel transgenic plants comprising CryI
CC delta-endotoxin genes, in particular cryIC genes that encode modified
CC crystal proteins having improved resistance to Lepidopteran insects. The
CC plants that express the mutated CryIC delta-endotoxin crystal proteins
CC are monocotyledonous (corn, wheat, oat, rice, barley, turf grass, pasture
CC grass) or dicotyledonous (legume, soybean, cotton, fruit, berry, tree).
CC The present sequence is a DNA encoding *Bacillus thuringiensis* CryIC-R148A
CC mutant protein.
XX
XX Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;
SQ
Query Match 89.6%; Score 2429.4; DB 24; Length 3567;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 241 ATGCGAGAAATTAATCAAAATCAATGCATACCTTCAATGTTTAAAGTAATCTCGAAGAA 300
DB 1 ATGCGAGAAATTAATCAAAATCAATGCATACCTTCAATGTTTAAAGTAATCTCGAAGAA 60
QY 301 GTACTTTTGGATGGAGACCGGATATCAACTGGTAATTAATCTCAATTCATATTTCTCTGTC 360
DB 61 GTACTTTTGGATGGAGACCGGATATCAACTGGTAATTAATCTCAATTCATATTTCTCTGTC 120
QY 361 CTGTGTTTCAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGATTAATA 420
DB 121 CTGTGTTTCAGTTTCTGGTATCTAACTTTGTACAGGGGGAGGATTTTGTAGTTGATTAATA 180
QY 421 GATTTTGTATGGGAATAGTTGGCCCTCTCAATGGGATGCAATTTCTAGTACAAATGAA 480
DB 181 GATTTTGTATGGGAATAGTTGGCCCTCTCAATGGGATGCAATTTCTAGTACAAATGAA 240
QY 481 CAATTAATTAATGAAAGATAGCTGAATTTGCTAGGAATGCTGCTAATTTAGAA 540
DB 241 CAATTAATTAATGAAAGATAGCTGAATTTGCTAGGAATGCTGCTAATTTAGAA 300
QY 541 GGAATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGATCCT 600
DB 301 GGAATTAGGAAACAAATTTCAATATATATGTGGAAGCAATTTAAAGAAATGGGAAGATCCT 360
QY 601 AATATCCAGCAACCAAGGACCGAGTAATGTATGATCGCTTTGCTATATCTGATGGGCTACTT 660
DB 361 AATAATCCAGCAACCAAGGACCGAGTAATGTATGATCGCTTTGCTATATCTGATGGGCTACTT 420
QY 661 GAAAGGGACATTCCTTCGTTTCGAATTTCTGGATTTGAGTACCCCTTTTATCCGTTTAT 720
DB 421 GAAAGGGACATTCCTTCGTTTCGAATTTCTGGATTTGAGTACCCCTTTTATCCGTTTAT 480
QY 721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780
DB 481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540
QY 781 TTGGGATTCGAAACGATAATGTCAATGAAACTATAATAGACTAATTAGGCATATGAT 840
DB 541 TGCGGATTCGAAACGATAATGTCAATGAAACTATAATAGACTAATTAGGCATATGAT 600
QY 841 GAATATGCTGATCAGTCTGCAATAGCTATATTCGGGGATTAATTAATTTACCGAAATCT 900
DB 601 GAATATGCTGATCAGTCTGCAATAGCTATATTCGGGGATTAATTAATTTACCGAAATCT 660
QY 901 ACCTATCAAGATTGGATAACATATAATCGATTACGGAGAGACTTTAACTTTGATCTGATTA 960
DB 661 AGGATCAAGATTGGATAACATATAATCGATTACGGAGAGACTTTAACTTTGATCTGATTA 720
QY 961 GATATGCCCGCTTTCTTTCCAAACTATATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT 1020

DB 721 GATATGCCCGCTTTCTTTCCAAACTATAGAGATATCCAAATTCAGCCAGTTGGT 780
QY 1021 CAACTAAAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTTACAGTCT 1080
DB 781 CAACTAAAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTTACAGTCT 840
QY 1081 GTAGCTCAATTAACCTACTTTTAAACGTTATGGAGAGCAGCGCAATTAAGAAATCTCATTTA 1140
DB 841 GTAGCTCAATTAACCTACTTTTAAACGTTATGGAGAGCAGCGCAATTAAGAAATCTCATTTA 900
QY 1141 TTGATATATGAATTAATCTTACAATCTTTACCGATTTGTTAGTGTGGAGCCGAATTTT 1200
DB 901 TTGATATATGAATTAATCTTACAATCTTTACCGATTTGTTAGTGTGGAGCCGAATTTT 960
QY 1201 TATTTGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGGTGGTAACATCTCCT 1260
DB 961 TATTTGGGAGGACATCGAGTAATATCTAGCCTTTATAGGAGGTGGTAACATCTCCT 1020
QY 1261 ATATATGGAAGAGAGCGGAAACAGGAGCCTCCAAGATCTCTTACTTTTAAATGACCGGTA 1320
DB 1021 ATATATGGAAGAGAGCGGAAACAGGAGCCTCCAAGATCTCTTACTTTTAAATGACCGGTA 1080
QY 1321 TTTAGGACTTTTACAATCTTACTTACGATTTATTAACGAACTTTGCGCAGCCACCAT 1380
DB 1081 TTTAGGACTTTTACAATCTTACTTACGATTTATTAACGAACTTTGCGCAGCCACCAT 1140
QY 1381 TTTAAATTTACGTTGGTGAAGGAGTAGAATTTCTTACACCTTACAAATAGCTTTACGTAT 1440
DB 1141 TTTAAATTTACGTTGGTGAAGGAGTAGAATTTCTTACACCTTACAAATAGCTTTACGTAT 1200
QY 1441 GCAGGAAGAGGTACGTTGATTTCTTTAACTGAATTTACCGCTTGAGGATTAATAGTGTGCCA 1500
DB 1201 CGAGGAAGAGGTACGTTGATTTCTTTAACTGAATTTACCGCTTGAGGATTAATAGTGTGCCA 1260
QY 1501 CTTCCGGAAGGATATAGTCAATCGTTTATGTCATGCAACTTTTGTTCAGAAAGTCTGAAACA 1560
DB 1261 CTTCCGGAAGGATATAGTCAATCGTTTATGTCATGCAACTTTTGTTCAGAAAGTCTGAAACA 1320
QY 1561 CTTTCTTTTAAACAACGTTGTAGTATTTCTTGGAGCAGTCTGAGTGCACCTCTTACAAAT 1620
DB 1321 CTTTCTTTTAAACAACGTTGTAGTATTTCTTGGAGCAGTCTGAGTGCACCTCTTACAAAT 1380
QY 1621 ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG 1680
DB 1381 ACAATTTGATCCAGAGAGAAATTAATCAAAATACCTTTTAGTGAAGGATTTAGAGTTTGGGG 1440
QY 1681 GGCACCTCTGTCTATTAACGAGCACGATTTTACAGGAGGATATCTTTCGAAAGAAATACC 1740
DB 1441 GGCACCTCTGTCTATTAACGAGCACGATTTTACAGGAGGATATCTTTCGAAAGAAATACC 1500
QY 1741 TTTTGGTGTATTTGTATCTCTCAAGTCTAATTAATTCACCAATTTACCCCAAGATACCTT 1800
DB 1501 TTTTGGTGTATTTGTATCTCTCAAGTCTAATTAATTCACCAATTTACCCCAAGATACCTT 1560
QY 1801 TTAAGATTTTCGTACGCTTCCAGTAGGATGACAGAGTTATAGTATTAACAGAGCGGCA 1860
DB 1561 TTAAGATTTTCGTACGCTTCCAGTAGGATGACAGAGTTATAGTATTAACAGAGCGGCA 1620
QY 1861 TCCACAGAGTGGGAGGCCAAGTTAGTGTAAATATGCTCTTTCAGAAAACTATGGAATA 1920
DB 1621 TCCACAGAGTGGGAGGCCAAGTTAGTGTAAATATGCTCTTTCAGAAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTAAATCTTTTTCATTT 1980
DB 1681 GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTAAATCTTTTTCATTT 1740
QY 1981 AGAGCTAAATCCAGATATTAATTTGGGATAAGTGAACCACTCTTATTTGGTGCAGGTTCTAT 2040
DB 1741 AGAGCTAAATCCAGATATTAATTTGGGATAAGTGAACCACTCTTATTTGGTGCAGGTTCTAT 1800
QY 2041 AGTAGCTTGAATCTTTTATATAGATAAAATTTGAAATTTTCTTAGCAGATGCAACATTTGAA 2100

XX	21-JUN-1999;	99US-0337635.
PF		
XX	26-NOV-1997;	97US-0980071.
PR		
XX	27-NOV-1996;	96US-0757536.
PA	(MONS) MONSANTO TECHNOLOGY LLC.	
XX	Baum JA, Gilmer AJ, Mettius AL;	
PI		
XX	WPI; 2002-033341/04.	
DR	P-PSDB; AAE26465.	
XX	Transgenic plants, comprises nucleic acid encoding CryIc	
PT	delt toxin polypeptide, has improved resistance to Lepidopteran	
FT	insects -	
XX	Disclosure; Column 201-210; 151pp; English.	
PS	The present invention relates to novel transgenic plants comprising CryI	
XX	delt toxin genes, in particular cryII genes that encode modified	
CC	crystal proteins having improved resistance to lepidopteran insects. The	
CC	plants that express the mutated cryII delta-endotoxin crystal proteins	
CC	are monocotyledonous (corn, wheat, oat, rice, barley, turf grasses, pasture	
CC	grasses) or dicotyledonous (legume, soybean, cotton, fruit, berry, tree).	
CC	The present sequence is Bacillus thuringiensis CRYIC.499 mutant DNA.	
XX	Sequence 3567 BP; 1167 A; 599 C; 791 G; 1010 T; 0 other;	
QY	Query Match	89.6%; Score 2429.8; DB 24; Length 3567;
Dd	Best Local Similarity	98.9%; Pred. No. 0;
QY	Matches 2445; Conservative	0; Mismatches 26; Indels 0; Gaps 0;
QY	241 ATGAGGAAAAAATAATCAAAATCAATGCATACCTTACAATTGTTTAAAGTAATCCTGAAGA	300
Dd	1 ATGAGGAAAAAATAATCAAAATCAATGCATACCTTACAATTGTTTAAAGTAATCCTGAAGA	60
QY	301 GTACTTTTGATGGAGAACGGATATCAACTGGTAAATTAATCAATTCATATTTCTCTGTCA	360
Dd	61 GTACTTTTGATGGAGAACGGATATCAACTGGTAAATTAATCAATTCATATTTCTCTGTCA	120
QY	361 CTCTCTCAGTTTCTGTATCTAACTTTGTACCAGGGGAGGATTTTTAGTTGGATTAATA	420
Dd	121 CTCTCTCAGTTTCTGTATCTAACTTTGTACCAGGGGAGGATTTTTAGTTGGATTAATA	180
QY	421 GATTTTGTATGGGATATGTGGCCCTTCTCAATGGATGCAATTTCTAGTACAAAATCGAA	480
Dd	181 GATTTTGTATGGGATATGTGGCCCTTCTCAATGGATGCAATTTCTAGTACAAAATCGAA	240
QY	481 CAATTAATTAATGAAGATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA	540
Dd	241 CAATTAATTAATGAAGATAGCTGAATTTGCTAGGAATGCTGCTATTGCTAATTTAGAA	300
QY	541 GGATAGGAAACAAATTTCAATATATATGCGAGCAATTAAGATCGGAAGAAGATCTT	600
Dd	301 GGATAGGAAACAAATTTCAATATATATGCGAGCAATTAAGATCGGAAGAAGATCTT	360
QY	601 AATAATCAGAACACAGGACAGGATTAATGATCGCTTTGCTATATCTTGATGGCTACTT	660
Dd	361 CATTAATCAGAACACAGGACAGGATTAATGATCGCTTTGCTATATCTTGATGGCTACTT	420
QY	661 GAAAGGACATTTCTGGTTTCGAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTAT	720
Dd	421 GAAAGGACATTTCTGGTTTCGAATTTCTGGATTTGAAGTACCCCTTTTATCCGTTTAT	480
QY	721 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTATATTTTGGAGAAAG	780
Dd	481 GCTCAAGCGGCCAATCTGCATCTAGCTATATTAAGAGATTCGTATATTTTGGAGAAAG	540
QY	781 TTGGGATTTGACACGATTAATGCAATGAAACCTATATAGACTAATTAGCATATTTGAT	840
Dd	541 TGCGGATTTGACACGATTAATGCAATGAAACCTATATAGACTAATTAGCATATTTGAT	600

1801 AGTAGCGGTGAACCTTTATATAGATAAAATTTCAAATTTATTTAGCAGATCGAATTTGAA 1860

2101 GCAGAACTCTGATTTAGAGAGACACAAAGGCGGTGAATGCCCTGTGTTTACTTCTTCCAAAT 2160

1861 GCAGAACTCTGATTTAGAGAGACACAAAGGCGGTGAATGCCCTGTGTTTACTTCTTCCAAAT 1920

2161 CAATTCGGGTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 2220

1921 CAATTCGGGTTAAAAACCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTG 1980

2221 GATTTGTTATCAGATCAATTTTGTCTGATGAAAGCGGAGATTTGTCGAGAAAGTCAAA 2280

1981 GATTTGTTATCAGATCAATTTTGTCTGATGAAAGCGGAGATTTGTCGAGAAAGTCAAA 2040

2281 CATGCGAGGATCTCAGTGTACGACGGATTTTACTTCAAGATCCAAATTTCAAGGGATC 2340

2041 CATGCGAGGATCTCAGTGTACGACGGATTTTACTTCAAGATCCAAATTTCAAGGGATC 2100

2341 AATAGACACCGACCGTGGCTGAGAGGAGTACAGATATTAATCAATCCAAAGGAGAT 2400

2101 AATAGACACCGACCGTGGCTGAGAGGAGTACAGATATTAATCAATCCAAAGGAGAT 2160

2401 GAGGTATTTCAAGGAAATTTAGTGTACATCACCGGTACCGTTGATGAGTCTATCCAAG 2460

2161 GAGGTATTTCAAGGAAATTTAGTGTACATCACCGGTACCGTTGATGAGTCTATCCAAG 2220

2461 TATTTATATCAAGAAATPAGATGAGTGTGAAATTAAGATTTATACCGTGTATGAAATAGA 2520

2221 TATTTATATCAAGAAATPAGATGAGTGTGAAATTAAGATTTATACCGTGTATGAAATAGA 2280

2521 GGGTATATCGAAGATAGTCAAGATTTAGAAATCTATTTGATCGGTACATGCAAAACAC 2580

2281 GGGTATATCGAAGATAGTCAAGATTTAGAAATCTATTTGATCGGTACATGCAAAACAC 2340

2581 GAAATAGTAAATGTGCCAGGACACGGTTTCTTTATGGCGGTTTTCAGCCCAAGTCCAAATC 2640

2341 GAAATAGTAAATGTGCCAGGACACGGTTTCTTTATGGCGGTTTTCAGCCCAAGTCCAAATC 2400

2641 GGAAGTGTGGAGAACCGAATCGATGCGCGGCACACCTTGAATGGAATCTGATCTAGAT 2700

2401 GGAAGTGTGGAGAACCGAATCGATGCGCGGCACACCTTGAATGGAATCTGATCTAGAT 2460

2701 TGTTCCTGCGAG 2711

2461 TGTTCCTGCGAG 2471

RESULT 14

AAD44215 standard; DNA; 3567 BP.

ID AAD44215

AC AAD44215;

DT 13-DEC-2002 (first entry)

XX Bacillus thuringiensis CRYIC.499 mutant DNA.

DE Bacillus thuringiensis CRYIC.499 mutant insect;

KW CryI protein; delta-endotoxin; insect resistance; lepidopteran insect;

RW transgenic plant; transgenic; mutant; gene; ds.

XX Bacillus thuringiensis.

OS Synthetic.

Key Location/Qualifiers

CDS 1..3567

FT /*tag= a

FT /product= "CRYIC.499 mutant protein"

FT /note= "No stop codon".

FT /partial

XX US6313378-B1.

XX 06-NOV-2001.

PD

Qy	841	GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATAATTTACCGAAATCT	900
Db	601	GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATAATTTACCGAAATCT	660
Qy	901	ACGTATCAAGATTGATTAACATATAATTCGATTACGGAGAGACTTAAACATTGACATCTGTATT	960
Db	661	ACGTATCAAGATTGATTAACATATAATTCGATTACGGAGAGACTTAAACATTGACATCTGTATT	720
Qy	961	GATATCGCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT	1020
Db	721	GATATCGCGCGCTTTCTTTCCAAACTATGACAAATAGGAGATATCCAAATTCAGCCAGTTGGT	780
Qy	1021	CAACTAACAGGGGAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCT	1080
Db	781	CAACTAACAGGGGAAGTTTATACGGACCCATTAATTAATTTTAATCCACAGTTACAGTCT	840
Qy	1081	GTAGCTCAATTAACCTACTTTTAAAGTTATGAGAGAGCGCGCAATAGAAATCTCAATTT	1140
Db	841	GTAGCTCAATTAACCTACTTTTAAAGTTATGAGAGAGCGCGCAATAGAAATCTCAATTT	900
Qy	1141	TTTGATATATTGAATAATCTTTACCAATCTTTACGGATTGGTTTAGTTTGGACGCAATTTT	1200
Db	901	TTTGATATATTGAATAATCTTTACCAATCTTTACGGATTGGTTTAGTTTGGACGCAATTTT	960
Qy	1201	TATTGGGGAGGACATCGAGTAAATATCTAGCCCTTATAGAGGTGTATAACAATCTCCT	1260
Db	961	TATTGGGGAGGACATCGAGTAAATATCTAGCCCTTATAGAGGTGTATAACAATCTCCT	1020
Qy	1261	ATATATCGAAGAGAGCGGACACGAGGCGCTCCAAGATCCTTTACTTTTATAGACCGGTA	1320
Db	1021	ATATATCGAAGAGAGCGGACACGAGGCGCTCCAAGATCCTTTACTTTTATAGACCGGTA	1080
Qy	1321	TTTAGGACTTTATCAATTCCTACTTTTACGATTATTACAGCAACTCTGCAGCGCCACAT	1380
Db	1081	TTTAGGACTTTATCAATTCCTACTTTTACGATTATTACAGCAACTCTGCAGCGCCACCA	1140
Qy	1381	TTTAAATTTTACGTGTGTGAAGGAGTAAATTTTCTACACTACAAATAGCTTTTACGTAT	1440
Db	1141	TTTAAATTTTACGTGTGTGAAGGAGTAAATTTTCTACACTACAAATAGCTTTTACGTAT	1200
Qy	1441	GCAGAGAGAGTACGGTTGATTCTTTAACTGAAATACGGCTGAGGATTAATAGTGTCCA	1500
Db	1201	GCAGAGAGAGTACGGTTGATTCTTTAACTGAAATACGGCTGAGGATTAATAGTGTCCA	1260
Qy	1501	CCTCGCAAGGATATAGTCATCGTTTATGTCAATCAACTTTTGTTCAGAGATCTGGAACA	1560
Db	1261	CCTCGCAAGGATATAGTCATCGTTTATGTCAATCAACTTTTGTTCAGAGATCTGGAACA	1320
Qy	1561	CTTTTTTTAACTCGTGTAGTATTTTCTTGGACGATCGTAGTCAACTCTTACAAAT	1620
Db	1321	CTTTTTTTAACTCGTGTAGTATTTTCTTGGACGATCGTAGTCAACTCTTACAAAT	1380
Qy	1621	ACAATTCATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGGATTTAGAGTTGGGG	1680
Db	1381	ACAATTCATCCAGAGAGAAATTAATCAATACCTTTAGTGAAGGATTTAGAGTTGGGG	1440
Qy	1681	GGCACCTCTGTCAATTACAGGACCAAGATTTACAGGAGGGGATATCCCTTCAGAGAAATACC	1740
Db	1441	GGCACCTCTGTCAATTACAGGACCAAGATTTACAGGAGGGGATATCCCTTCAGAGAAATACC	1500
Qy	1741	TTTGGTGATTTTGTATCTCTACAAAGTCAATTAATTAATTCACCAATTCACCAAGATACCGT	1800
Db	1501	TTTGGTGATTTTGTATCTCTACAAAGTCAATTAATTAATTCACCAATTCACCAAGATACCGT	1560
Qy	1801	TTAAGATTTTGGTTACGCTTCCAGTAGGGATGACAGCAGTTATAGTATTTAAACAGAGCGGCA	1860
Db	1561	TTAAGATTTTGGTTACGCTTCCAGTAGGGATGACAGCAGTTATAGTATTTAAACAGAGCGGCA	1620
Qy	1861	TCCACAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA	1920
Db	1621	TCCACAGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCAGAAAACTATGGAATA	1680
Qy	1921	GGGGAGAACTTAACTCTAGAACATTTAGATATACCGATTTTAGTATCTCTTTTCAATTT	1980

Db	1681	GGGAGAACTTAA	CATCTAGAACATT	TAGATATACCGATTTTAGTAATCCTTTTTCAATTT	1740
Qy	1981	AGAGCTAATCCAGATA	TAAATTTGGGATAAGTGAAACAACCTCATTTTGGTGAGGTTCTATT	2040	
Db	1741	AGAGCTAATCCAGATA	TAAATTTGGGATAAGTGAAACAACCTCATTTTGGTGAGGTTCTATT	1800	
Qy	2041	AGTAGCGTTGAAC	TTTATATAGATAAAAATGAAATTAATCTTAGCAGATGCAACATTTGAA	2100	
Db	1801	AGTAGCGGTGAAC	TTTATATAGATAAAAATGAAATTAATCTTAGCAGATGCAACATTTGAA	1860	
Qy	2101	GCAGAATCTGATTT	PAGAAAGAGCAAAAAGCGCGTGAAATCCCTGTTTACTTCTTCCAAT	2160	
Db	1861	GCAGAATCTGATTT	PAGAAAGAGCAAAAAGCGCGTGAAATCCCTGTTTACTTCTTCCAAT	1920	
Qy	2161	CAAAATCGGGTTAAAAA	CCGATGTGACCGGATTATCATATTGATCNAAGTATCCAATTTAGTG	2220	
Db	1921	CAAAATCGGGTTAAAAA	CCGATGTGACCGGATTATCATATTGATCNAAGTATCCAATTTAGTG	1980	
Qy	2221	GATTTGTTTTATCAGAT	GAAATTTTGTCTCGATGAAAAGCGAGAAATTTGCCGAGAAAGTCAAA	2280	
Db	1981	GATTTGTTTTATCAGAT	GAAATTTTGTCTCGATGAAAAGCGAGAAATTTGCCGAGAAAGTCAAA	2040	
Qy	2281	CATCGAAGCGACT	CAGTGATGAGCGGAAATTTACTTCCAAGATCCAACTTCAGAGGGATC	2340	
Db	2041	CATCGAAGCGACT	CAGTGATGAGCGGAAATTTACTTCCAAGATCCAACTTCAGAGGGATC	2100	
Qy	2341	AATAGACAAACAGAC	CCGTGGCTGGAGAGGAGTACAGATATTACCATTCCAAGAGGAGAT	2400	
Db	2101	AATAGACAAACAGAC	CCGTGGCTGGAGAGGAGTACAGATATTACCATTCCAAGAGGAGAT	2160	
Qy	2401	GACGTATTTCAAAGAGA	ATTACGTACACTACCGGTACCGTTGATGAGTGCTATCCAACG	2460	
Db	2161	GACGTATTTCAAAGAGA	ATTACGTACACTACCGGTACCGTTGATGAGTGCTATCCAACG	2220	
Qy	2461	TATTTATATCAGAAAAT	TAGATGAGTGCAGAAATTTAAAAGCTTTATACCCGTTATGAATTAAGA	2520	
Db	2221	TATTTATATCAGAAAAT	TAGATGAGTGCAGAAATTTAAAAGCTTTATACCCGTTATGAATTAAGA	2280	
Qy	2521	GGGTATATCGAAGAT	TAGTCAAGACTTAGAATCTATTTTGATCGGGTACAAATGCAAAACAC	2580	
Db	2281	GGGTATATCGAAGAT	TAGTCAAGACTTAGAATCTATTTTGATCGGGTACAAATGCAAAACAC	2340	
Qy	2581	GAAATAGTAAATGTGCC	AGCACGGGTTCCCTATGCGCGCTTTTTCAGCCCCAAAGTCCCAATC	2640	
Db	2341	GAAATAGTAAATGTGCC	AGCACGGGTTCCCTATGCGCGCTTTTTCAGCCCCAAAGTCCCAATC	2400	
Qy	2641	GGAAAGTGTGGAGAAC	CGAATCGATGCGCGCCACACCTTTGAATGGGAATCCTGATCTAGAT	2700	
Db	2401	GGAAAGTGTGGAGAAC	CGAATCGATGCGCGCCACACCTTTGAATGGGAATCCTGATCTAGAT	2460	
Qy	2701	TGTTCTCTGCAG	2711		
Db	2461	TGTTCTCTGCAG	2471		

RESULT 15

ABS70781
ID ABS70781 standard; DNA; 3567 BP.

AC ABS70781;

DT 26-NOV-2002 (first entry)

DE B. thuringiensis DNA encoding CRY mutant Cry1C-R148A

Crystal protein; CRY1C; ds; gene; mutant; delta-endotoxin; insecticide; lepidopteran insect.

XX OS Bacillus thuringiensis.

US Bacillus thuringiensis
OS Synthetic.

XX PN US6423828-B1

XX PD 23-JUL-2002.

XX PF 22-JUN-1999; 99US-0337280.

XX PR 26-NOV-1997; 97US-0980071.

XX PR 27-NOV-1996; 96US-0757536.

XX PA (MONS) MONSANTO TECHNOLOGY LLC.

XX PA Baum JA, Gilmer AJ, Mettius AL;

XX PI WPI; 2002-705183/76.

XX DR P-PSDB; ABG93814.

XX PT New delta endotoxin polypeptides, which are Lepidopteran-toxic

XX PT polypeptides, useful as an insecticide, particularly for killing

XX PT Lepidopteran insects or insect cells.

XX PS Example 5; Column 105-108; 149pp; English.

XX PS The invention relates to an isolated CryIcA* delta-endotoxin polypeptide

XX CC useful as an insecticide. CryIcA* is a crystal protein from *B. thuringiensis*.

XX CC The isolated CryIcA* delta-endotoxin polypeptide comprises

XX CC (a) one or more amino acid mutations in the loop regions between alpha

XX CC helices 4 and 5 of domain 1; (b) one or more amino acid mutations in the

XX CC loop region between alpha helices 6 and 7 of domain 1; or (c) has

XX CC improved activity against lepidopteran insects relative to a native CryIc

XX CC delta-endotoxin polypeptide. The CryIcA* delta-endotoxin polypeptide is

XX CC useful as an insecticide, particularly for killing lepidopteran insects

XX CC or insect cells. The present sequence encodes a mutant CryIc protein of

XX CC the invention.

XX SQ Sequence 3567 BP; 1168 A; 597 C; 791 G; 1011 T; 0 other;

Query Match 89.6%; Score 2429.4; DB 24; Length 3567;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 241 ATGGAGGAAATATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAA 300

DB 1 ATGGAGGAAATATCAAAATCAATGCATACCTTACAAATGTTTAAAGTAATCTCTGAAGAA 60

QY 301 GTACTTTTGGATGGAGAACGGATATCACTGGTAATTTACTCAATGATATTTCTCTGTCA 360

DB 61 GTACTTTTGGATGGAGAACGGATATCACTGGTAATTTACTCAATGATATTTCTCTGTCA 120

QY 361 CTGTGTCAGTTCTTGATATCTACTTTGTACAGGGGAGGATTTTATGTTGATTAATA 420

DB 121 CTGTGTCAGTTCTTGATATCTACTTTGTACAGGGGAGGATTTTATGTTGATTAATA 180

QY 421 GATTTGTTATGGGAATAGTTGGCCCTTCAATGGGATGCAATTCATGACAAATGGA 480

DB 181 GATTTGTTATGGGAATAGTTGGCCCTTCAATGGGATGCAATTCATGACAAATGGA 240

QY 481 CAATTAATTAATGAAGAATAGTCTGTAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 540

DB 241 CAATTAATTAATGAAGAATAGTCTGTAATTTGCTAGGAATGCTGCTATTTGCTAATTTAGAA 300

QY 541 GGAATTAGGAAACAATTTCAATATATATGTGGAAGCATTTAAAGAATGGGAAGAATCT 600

DB 301 GGAATTAGGAAACAATTTCAATATATATGTGGAAGCATTTAAAGAATGGGAAGAATCT 360

QY 601 AATAATCCAGCAACACAGAACAGAGTAATTTGATCGCTTTTCGTATATCTTATGATGGGCTACTT 660

DB 361 AATAATCCAGCAACACAGAACAGAGTAATTTGATCGCTTTTCGTATATCTTATGATGGGCTACTT 420

QY 661 GAAAGGACAAATTTCTGTTTCCGAATTTCTGGATTTGCAAGTACCCCTTTTATCCGTTTAT 720

DB 421 GAAAGGACAAATTTCTGTTTGGCAATTTCTGGATTTGCAAGTACCCCTTTTATCCGTTTAT 480

QY 721 GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 780

DB 780

DB 481 GCTCAAGCGGCAATCTGCAATCTAGCTATATTAAGAGATTTCTGTAATTTTGGAGAAAGA 540

QY 781 TTGGGATTTGCAACGATTAATGTCAATGAAGACTATTAATAGACTATTAAGCANTATTGAT 840

DB 541 TGGGGATTTGCAACGATTAATGTCAATGAAGACTATTAATAGACTATTAAGCANTATTGAT 600

QY 841 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATTTTACCGAATCT 900

DB 601 GAATATGCTGATCACTGTGCAAAATACGTATTAATCGGGGATTAATAATTTTACCGAATCT 660

QY 901 ACGTATCAAGATTGGATAACAATATAATCGATTAACGAGAGACTTAACATGACTGTATTA 960

DB 661 ACGTATCAAGATTGGATAACAATATAATCGATTAACGAGAGACTTAACATGACTGTATTA 720

QY 961 GATATCGCCGCTTTCTTTTCCAAACTATGACAAATAGGAGATATCCAATTCAGCCAGTTGGT 1020

DB 721 GATATCGCCGCTTTCTTTTCCAAACTATGACAAATAGGAGATATCCAATTCAGCCAGTTGGT 780

QY 1021 CAACTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 1080

DB 781 CAACTAACAGGGAAGTTTATACGGACCCATTAATTAATTTTAAATCCACAGTTACAGTCT 840

QY 1081 GTAGCTCAATTAACCTACTTTTAAAGTTTATGGAGAGCAGCCAAATAGAATCTCTCAATTTA 1140

DB 841 GTAGCTCAATTAACCTACTTTTAAAGTTTATGGAGAGCAGCCAAATAGAATCTCTCAATTTA 900

QY 1141 TTTGATATATCGAATAATCTTACAACTTTTACAGGATGTTTATGTTAGTGTGAGCGCAATTTT 1200

DB 901 TTTGATATATCGAATAATCTTACAACTTTTACAGGATGTTTATGTTAGTGTGAGCGCAATTTT 960

QY 1201 TATTTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGTGTGTAACATACATCTCTCT 1260

DB 961 TATTTGGGAGGACATCGAGTAATATCTAGCCCTTATAGGAGTGTGTAACATACATCTCTCT 1020

QY 1261 ATATATGGAAGAGAGCGGCAACAGGAGCCTCCAAGATCTTTTACTTTTAAATGGACCGGTA 1320

DB 1021 ATATATGGAAGAGAGCGGCAACAGGAGCCTCCAAGATCTTTTACTTTTAAATGGACCGGTA 1080

QY 1321 TTTAGGACTTTTATCAAAATCTCTACTTTTACGATTTATACAGCAACTTTGGCCAGCGCCACCA 1380

DB 1081 TTTAGGACTTTTATCAAAATCTCTACTTTTACGATTTATACAGCAACTTTGGCCAGCGCCACCA 1140

QY 1381 TTTAAATTTACGTGGTGTGGAAGGAGTAGAATTTTCTACACTCAAAATAGCTTTTACGAT 1440

DB 1141 TTTAAATTTACGTGGTGTGGAAGGAGTAGAATTTTCTACACTCAAAATAGCTTTTACGAT 1200

QY 1441 GCGAAGAGAGTACGGTTGATTTCTTTAACTGAATTAACCGCTGAGGATTAATAGTGTGCCA 1500

DB 1201 GCGAAGAGAGTACGGTTGATTTCTTTAACTGAATTAACCGCTGAGGATTAATAGTGTGCCA 1260

QY 1501 CCTCGCAAGAGATAGTATCATGCTTTATGTCACTCAACTTTTGTTCAAAGATCTCGAACA 1560

DB 1261 CCTCGCAAGAGATAGTATCATGCTTTATGTCACTCAACTTTTGTTCAAAGATCTCGAACA 1320

QY 1561 CTTTCTTTTACACTGGTGTAGTATTTTCTTGGACGATCTAGTGTCAACTCTTACAAAT 1620

DB 1321 CTTTCTTTTACACTGGTGTAGTATTTTCTTGGACGATCTAGTGTCAACTCTTACAAAT 1380

QY 1621 ACAATTCATCCAGAGAAATTAATCAAAATCTTTTATGTGAAAGATTTAGAGTTTGGGG 1680

DB 1381 ACAATTCATCCAGAGAAATTAATCAAAATCTTTTATGTGAAAGATTTAGAGTTTGGGG 1440

QY 1681 GCGACCTCTCTCATTTACAGGACAGGATTTACAGGGGGATATCTCTCGAAGAAATACC 1740

DB 1441 GCGACCTCTCTCATTTACAGGACAGGATTTACAGGGGGATATCTCTCGAAGAAATACC 1500

QY 1741 TTTGGTGAATTTGTATCTCTCAAGTCAATTAATTAATCAAAATTCACCAAGATACCGT 1800

DB 1501 TTTGGTGAATTTGTATCTCTCAAGTCAATTAATTAATCAAAATTCACCAAGATACCGT 1560

QY 1801 TTAAGATTTCTGTTACGCTTCCAGTAGGATTCAGACAGTATTATAGTATTAAACAGAGCGCA 1860

DB 1561 TTAAGATTTCTGTTACGCTTCCAGTAGGATTCAGACAGTATTATAGTATTAAACAGAGCGCA 1620

QY 1861 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAGATATGCTCTTCCAGAAAACTATGGAATA 1920
DB |||||
DB 1861 TCCACAGGAGTGGGAGGCCAAGTTAGTGTAAATATGCTCTTCCAGAAAACTATGGAATA 1680
QY 1921 GGGGAGAACTTAACTACTAGACATTTAGATACCGATTTAGTAAATCTCTTTTCATTT 1980
DB |||||
DB 1681 GGGGAGAACTTAACTACTAGACATTTAGATATACCGATTTAGTAAATCTCTTTTCATTT 1740
QY 1981 AGAGCTAAATCCAGATATAATGGGATAAGTGAACAACTCTATTTGGTCAGGTTCTATT 2040
DB |||||
DB 1741 AGAGCTAAATCCAGATATAATGGGATAAGTGAACAACTCTATTTGGTCAGGTTCTATT 1800
QY 2041 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTATCTAGCAGATGCAACATTTGAA 2100
DB |||||
DB 1801 AGTAGCGTTGAACTTTATATAGATAAAATTTGAAATTTATCTAGCAGATGCAACATTTGAA 1860
QY 2101 GCAGAACTCTGATTTAGAAAGAGCACAAAGGGCGTGAATGCCCTGTTTACTCTTCCAAAT 2160
DB |||||
DB 1861 GCAGAACTCTGATTTAGAAAGAGCACAAAGGGCGTGAATGCCCTGTTTACTCTTCCAAAT 1920
QY 2161 CAAATCGGGTTAAAAACCGATGTGAGCGATTTATCATATTGATCAAGTATCCAAATTTAGTG 2220
DB |||||
DB 1921 CAAATCGGGTTAAAAACCGATGTGAGCGATTTATCATATTGATCAAGTATCCAAATTTAGTG 1980
QY 2221 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAAA 2280
DB |||||
DB 1981 GATTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAAA 2040
QY 2281 CATCGAAGCGACTAGTGTAGCGGAAATTTACTTCAAGATCCAACTTCAGAGGGATC 2340
DB |||||
DB 2041 CATCGAAGCGACTAGTGTAGCGGAAATTTACTTCAAGATCCAACTTCAGAGGGATC 2100
QY 2341 AATAGACAACGACCGTGGCTGGAGAGAGTACAGATATTACCATCCAAGGAGGAGAT 2400
DB |||||
DB 2101 AATAGACAACGACCGTGGCTGGAGAGAGTACAGATATTACCATCCAAGGAGGAGAT 2160
QY 2401 GACGTATTCAAAGAGAAATACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAACG 2460
DB |||||
DB 2161 GACGTATTCAAAGAGAAATACGTCACTACCGGGTACCGTTGATGAGTGCTATCCAACG 2220
QY 2461 TATTTATATCAGAAATAGATGATCGAAATTTAAAGCTTTATACCGTTATGAATTAAGA 2520
DB |||||
DB 2221 TATTTATATCAGAAATAGATGATCGAAATTTAAAGCTTTATACCGTTATGAATTAAGA 2280
QY 2521 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTTCATCGGTACAAATGCAAAACAC 2580
DB |||||
DB 2281 GGGTATATCGAAGATAGTCAAGACTTAGAAATCTATTTCATCGGTACAAATGCAAAACAC 2340
QY 2581 GAAATAGTAAATGTGCCAGCAGCGGTTCTTTATGGCCGCTTTACGCCAAAGTCCAATC 2640
DB |||||
DB 2341 GAAATAGTAAATGTGCCAGCAGCGGTTCTTTATGGCCGCTTTACGCCAAAGTCCAATC 2400
QY 2641 GGAAGTGTGGAAACCGAATCGATCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2700
DB |||||
DB 2401 GGAAGTGTGGAAACCGAATCGATCGCGCCACACCTTTGAATGGAATCCTGATCTAGAT 2460
QY 2701 TGTTCCTGCAG 2711
DB |||||
DB 2461 TGTTCCTGCAG 2471

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Job time : 869 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2003, 03:40:26 ; Search time 12714 Seconds
(without alignments)
8723.140 Million cell updates/sec

Title: US-09-918-485-1
Perfect score: 2711
Sequence: 1 AGCTTCATAGATCTCAA.....GATCTAGATTGTCCTGCAG 2711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hcg_hum.*
- 31: em_hcg_inv.*
- 32: em_hcg_other.*
- 33: em_hcg_mus.*
- 34: em_hcg_pln.*
- 35: em_hcg_rod.*
- 36: em_hcg_mam.*
- 37: em_hcg_vrt.*
- 38: em_sy.*
- 39: em_higo_hum.*
- 40: em_higo_mus.*
- 41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2711	100.0	2711	6	AR022642 Sequence
2	2711	100.0	2711	6	ARI75979 Sequence
3	2696.6	99.5	2711	1	BTTOXDA
4	2696.2	99.5	2711	6	A00221
5	2696.2	99.5	2711	6	A10218
6	2671.6	98.5	4930	1	AF362020
7	2664	98.3	3903	6	A27642
8	2664	98.3	3923	6	A31099
9	2664	98.3	3923	6	AR032226
10	2659.2	98.1	3923	6	ARI25059
11	2470.6	91.1	3706	1	BTETOXD
12	2446.6	90.2	3646	1	AY078160
13	2431	89.7	3567	6	A43696
14	2431	89.7	3567	6	AR000001
15	2431	89.7	3567	6	ARI43374
16	2429.4	89.6	3567	6	ARI05485
17	2429.4	89.6	3567	6	ARI20161
18	2429.4	89.6	3567	6	ARI20166
19	2429.4	89.6	3567	6	ARI26159
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21	2429.4	89.6	3567	6	ARI77975
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ALIGNMENTS

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LOCUS 2711 bp
DEFINITION Sequence 1 from patent US 5792928.
ACCESSION AR022642
VERSION AR022642.1 GI:3976704
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2711)
AUTHORS Sanchis,V., Lereclus,D., Menou,G., Lecadet,M.-M., Martouret,D. and Dedonder,R.
TITLE Nucleotide sequences coding for polypeptides endowed with a larvicidal activity towards lepidoptera

linear PAT 05-DEC-1998

JOURNAL Patent: US 5792928-A 1 11-AUG-1998;

FEATURES Location/Qualifiers

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 Unclassified.
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 Dedonder,R.
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RESULT 5
A10218
LOCUS

A10218

2711 bp

DNA

linear

PAT 27-JAN-1994

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DEFINITION B.thuringiensis DNA for lepidoptera larvicidal protein.
 ACCESSION A10218
 VERSION A10218.1 GI:490198
 KEYWORDS
 SOURCE
 ORGANISM
 Bacillus thuringiensis
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
 REFERENCE 1 (bases 1 to 2711)
 AUTHORS Sanchis,V., Lereclus,D., Menou,G., Lecadet,M.M., Martouret,D. and Dedonder,R.
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 JOURNAL Patent: EP 0295156-A 1 14-DEC-1988;
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 KSTYQWITYNLRDLTLVLDIAAFPNVDNRYPIQVQLFREVYDPLNLP
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 Matches 2701; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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ORIGIN									
Query Match		98.5%	Score	2671.6;	DB 1;	Length	4930;		
Best Local Similarity		99.1%	Pred. No.	0;					
Matches 2686;		Conservative	0;	Mismatches	24;	Indels	0;	Gaps	0;
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QY	122	ATTGTTTACGTTTTTGTATTTTTTTCATAGATGTGTCATATGATTTTAAATCGTGTAAAT	181						
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DB	661	AAAGGACATTCCTTTCGTTTCGAAATTTCTGATTTGAAATTTGAAATTTTATCCGTTTATG	720						
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DB	1981	GAGCTTAATCCAGATATAATTTGGGATAAGTGAAACCTCTATTTGGTGGAGGTCTATTA	2040						
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A27642
LOCUS B.thuringiensis bt15 gene. 3903 bp DNA linear PAT 25-SBP-1995
DEFINITION B.thuringiensis bt15 gene.
ACCESSION A27642
VERSION A27642.1 GI:1247716
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE
1 (bases 1 to 3903)
AUTHORS Van Mellaert,H., Botterman,Johan., Van Rie,J. and Joos, Henk.
TITLE Prevention of Bt resistance development
JOURNAL Patent: EP 0400246-A 5 05-DEC-1990;
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Query Match 98.3%; Score 2664; DB 6; Length 3903;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2679; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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[illegible]

A31099
LOCUS A31099 3923 bp DNA linear PAT 16-JAN-1996
DEFINITION B.thuringiensis br15 gene from patent EP0408403.
ACCESSION A31099
VERSION A31099.1 GI:1247756
KEYWORDS
SOURCE Bacillus thuringiensis
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3923)
AUTHORS Van Mellaert, H., Botterman, J., Van Rie, J., and Joos, H.
TITLE Prevention of Bt resistance development
JOURNAL Patent: EP 0408403-A 3 16-JAN-1991;
PLANT GENETIC SYSTEMS, N.V.
FEATURES
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RESULT 9
AR032226
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

Sequence 4 from patent US 5866784.
AR032226
AR032226.1
GI:5946515

3923 bp
linear
PAT 29-SEP-1999

SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 3923)	
TITLE	Van Mellaert,H., Botterman,J., Van Rie,J. and Joos,H.	
JOURNAL	Recombinant plant expressing non-competitively binding insecticidal	
FEATURES	crystal proteins	
Location/Qualifiers	Patent: US 5866784-A 4 02-FEB-1999;	
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Query Match	98.3%; Score 2664; DB 6; Length 3923;	
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ARI25059

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

ARI25059
Sequence 7 from patent US 6172281.
linear PAT 16-MAY-2001

ARI25059.1
GI:14110453

Unknown.

Unclassified.

1 (bases 1 to 3923)

Van Mellaert H., Botterman J., Van Rie, J. and Joos, H.

Recombinant plant expressing non-competitively binding BT

insecticidal crystal proteins

Patent: US 6172281-A 7 09-JAN-2001;

Location/Qualifiers


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FEATURES
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3706 bp DNA linear BCT 12-SEP-1993
Bacillus thuringiensis gene for delta-endotoxin.
X07518 M37242
X07518.1 GI:40293
delta-endotoxin; endotoxin; insecticidal protein.
Bacillus thuringiensis
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus
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Honee, G., van der Salm, T. and Visser, B.
Nucleotide sequence of crystal protein gene isolated from B.
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Nucleic Acids Res. 16 (13), 6240 (1988)
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2 (bases 1 to 3706)
Honee, G.J.E.M.
Direct Submission
Submitted (02-MAY-1988) Honee G.J.E.M., ITAL, PO Box 48, 6700 AA,
Wageningen, The Netherlands
Location/Qualifiers
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AY078160 3646 bp DNA linear BCT 25-FEB-2002
Bacillus thuringiensis delta-endotoxin (cryIc) gene, complete cds.
AY078160 GI:18913152
Bacillus thuringiensis

ORGANISM. Bacillus thuringiensis
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 3646)
AUTHORS Kao S.-S. and Hsieh, F.-C.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2002) Biopesticide, Taiwan Agricultural Chemical and Toxic Substances Research Institute, COA, 11 Kuang Ming Road, Wu Feng, Taichung Hsien, Taiwan 413, Republic of China
Location/Qualifiers

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ORIGIN

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AUTHORS	Bosch, H. J. and Stiekema, W. J.		
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COMMENT	SANDOZ LTD (CH)		
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SOURCE Unknown.
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REFERENCE 1 (bases 1 to 3567)
AUTHORS Bosch, H. Jan. and Stiekema, W. Johannes.
TITLE Hybrid toxin
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Query Match 89.7%; Score 2431; DB 6; Length 3567;
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RESULT 15
LOCUS AR143374
DEFINITION Sequence 1 from patent US 6204246.
ACCESSION AR143374
VERSION AR143374.1 GI:15104660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 3567)
AUTHORS Bosch,H.Jan. and Stiekema,W.Johannes.
TITLE Hybrid toxin
JOURNAL Patent: US 6204246-A 1 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..3567
/organism="unknown"
BASE COUNT 1168 a 596 c 792 g 1011 t
ORIGIN
Query Match 89.7%; Score 2431; DB 6; Length 3567;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2446; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Search completed: October 13, 2003, 08:17:12
Job time : 12731 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:11:34 ; Search time 114 Seconds
(without alignments)
1862.959 Million cell updates/sec

Title: US-09-918-485-2

Perfect score: 4358

Sequence: 1 MEENNQOCIPYNCLSNPEE.....GEPNRCAPHLWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4287	98.4	1189	2	Q9L877
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3	2584	59.3	1160	2	Q93TF9
4	2530.5	58.1	1180	2	Q9S5V8
5	2525.5	58.0	1176	2	Q45736
6	2512.5	57.7	1176	2	Q9RC30
7	2403.5	55.2	1176	2	Q9S514
8	2371.5	54.4	1155	2	Q93T21
9	2368.5	54.3	1155	2	Q9F296
10	2356	54.1	1169	2	Q8GHE8
11	2355	54.0	1174	2	Q45749
12	2332	53.5	1177	2	Q85735
13	2332	53.5	1177	2	Q8GLY5
14	2330.5	53.5	1178	2	Q9R826
15	2328.5	53.4	1178	2	Q45768
16	2326	53.4	1177	2	Q03743

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18	2216.5	50.9	1118	2	Q9AM82
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20	1978	45.4	1228	2	Q93T75
21	1972	45.3	1228	2	Q93NM5
22	1834	42.1	1231	2	Q9S4B5
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26	1358.5	31.2	618	2	O32306
27	1354	31.1	618	2	O45737
28	1334.5	30.6	1144	2	Q8KZL7
29	1329.5	30.5	719	2	Q9F0P8
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31	1326.5	30.4	719	2	Q93NJ5
32	1326	30.4	1144	2	O45745
33	1325.5	30.4	719	2	O85796
34	1312.5	30.1	719	2	Q8KY61
35	1019.5	23.4	1280	2	Q8VUK9
36	974	22.3	1128	2	Q9FDC0
37	950	21.8	1236	2	Q939T3
38	913	20.9	181	2	O8GN55
39	912.5	20.9	652	2	Q9S6N9
40	906.5	20.8	297	2	O45789
41	892.5	20.5	645	2	Q9S603
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ALIGNMENTS

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Q9L877 ID Q9L877 PRELIMINARY; PRT; 1189 AA.
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DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Toxin CryIcA6.
GN CryIcA6.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;
RA Yu J., Pang Y., Li J.;
RT "Cloning and sequence analysis of the cryIcA6 gene from Bacillus thuringiensis, strain A2-F."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF215647; AAF37224.1; -
DR HSSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR Pfam; PF00555; endotoxin; 1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
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QY 721 DVFKENTVTLPGTVDECYPTLYYKIDESKLKAYTRYELRGYIHDSQDLEIYLIRYNAKH 780
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RESULT 2
ID O06894 PRELIMINARY; PRT: 1171 AA.
AC O06894;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cyt15a4.
CN Cyt15a4.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=LBIT-147;
RA Barboza-Corona J.E., Lopez-Meza J.E., Ibarra J.E.;
RT "Cloning and expression of the cyt15a4 gene of Bacillus thuringiensis
RL and the comparative toxicity of its gene product.";
RW World J. Microbiol. Biotechnol. 14:437-441(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=LBIT-147;
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RA Ibarra J.E., Barboza-Corona J.E.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94323; AAD04732.1; -.
DR HSP; P02965; 1CIY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR Pfam; PF00555; endotoxin_1.
DR Pfam; PF03944; endotoxin_C; 1.
DR Pfam; PF03945; endotoxin_N; 1.
SQ SEQUENCE 1171 AA; 133310 MW; 333603A1A782523A CRC64;

Query Match 61.4%; Score 2679; DB 2; Length 1171;
Best Local Similarity 64.4%; Pred No. 1.le-186;
Matches 555; Conservative 88; Mismatches 170; Indels 38; Gaps 15;

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Db 5 NQNOQVPYNCANPENEILDIR---SNSTVATNIALSIRLLASATPIGIGILLGLFDA 61
QY 63 VMGIVGPSQWDAFLVQIQEQLINERIAEFARNAANLGLGNFNFIYVAFKWEEDPNN 122
Db 62 IMGSGPQWDLFLEQIELLIDOKIEEFARNOALSRLEGISLDYGLYTEAFREWEADPTN 121
QY 123 PATRTRVIDRFRILDLGLLERDIPSRISGFEVPLLSVYQAANLHLAILRDSVIFGRWG 182
Db 122 PALKEMRTQFNDMNSILVTAIPLFSVQYQVPELSVYVQAANLHLSVLRDVSVFGWAG 181
QY 183 LTTINVENYNNRILRHIDEYADHCANTYKGLNLPKS-TYQDMITVYLRRLDLTLVL 241
Db 182 FDIATNGRYNDLRLLPIYTDYAVRWYNTGLRLPRTGLRNLWAFNQFRELITISVLD 241
QY 242 IAAFFPNYDNRRYPQVQGLTRVYTDPLINFPOLQSVAOQLPTFNWMESSAIRNPHLF 301
Db 242 IISFFPNYDSRLYPIPTSSQLTRVYTDVINITDYRVG----PSFENIENSAIRSPLM 297
QY 302 DIANNLTITFDWVSGVGRNFWGCHRVISLIGGN-ITSPYIGREANQEPFRSF---TFN 357
Db 298 DFLNNLTIDTD-LIRGVHYWACHRVTSHTFGSSQVITTPQYGNQNAEPRTIAPSTFP 355
QY 358 G--PVFTLSIPTLRLLQPCQRRHFNLRGEGVEFSTPTNS-FTYRGRGTVDLSITLPP 414
Db 356 GLNLFYRLSNPFRSENITPTLGINV--VQGVGFIOPNNAEVLRYSRGTVDLSNELPI 413
QY 415 E-DNSVPPREGYSHRLCHATFYORSGTTPFLTITGVWFSWTHRSATLNTIDPERINQIPLV 473
Db 414 DGENSL---VGYSHRLSHVLTSLNNTNITSLPTFWTHSATNTINPDIITQIPLV 470
QY 474 KGFVWGTGTSVITGPGFTGGLLRNTFGDPLVSLQVINSPIQRYRLFRYASSRDAKAV 533
Db 471 KGRFGGTSVITGPGFTGGLLRNTFGDPLVSLQVINSPIQRYRLFRYASSRDAKAV 530
QY 534 IVLTGAASTGVGGQVSNVNPLOKTMWIGENLTSTRTYTDPSNPFRANPDIIIGISEQ- 592
Db 531 TV-----AIGGQIRVDMTLEKTMWIGESLTSRTFTSTNPSFNPFRANPDIIIRIAEL 583
QY 593 PLFGAGSISSGELYIDKIEILADATFEASDLERAQKAVNALFTSSNOIGLKTVDVTH 652
Db 584 PIRG-----GELYIDKIEILADATFEEXDLERAQKAVNALFTSNOLGKTVDVTH 637
QY 653 IDQVSNLVDCLSDFCLEKRELSKVHAKLSDERNLQDNFNINQRPDRGWSGTDTIOGG 712
Db 638 IDQVSNLVECLSDFCLEKRELSKVHAKLSDERNLQDNFNINQRPDRGWSGTDTIOGG 697
QY 713 DITIQGDDVFKENYVTLPGTVDECYPTLYYKIDESKLKAYTRYELRGYIHDSQDLEIY 772
Db 698 DITIQGDDVFKENYVTLPGTVDECYPTLYYKIDESKLKAYTRYELRGYIHDSQDLEIY 757
QY 773 LIAYNAKHETLVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 758 LIRYNAKHETLVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 808
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:20:23 ; Search time 25 seconds
(without alignments)
1548.119 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNQICIPYNCLSPPE.....GEPNRCAPHEWNPDLDCSC 823

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4294	98.5	1189	1 CICA_BACTE	P05518 bacillus th
2	3495.5	80.2	1176	1 C1CB_BACTG	P56953 bacillus th
3	2680	61.5	1171	1 C1EA_BACTX	Q57458 bacillus th
4	2584	59.3	1160	1 C1DB_BACTU	Q45747 bacillus th
5	2573	59.0	1165	1 C1DA_BACTA	P19415 bacillus th
6	2564.5	58.8	1167	1 C1JA_BACTU	Q45738 bacillus th
7	2518.5	57.8	1176	1 C1AA_BACTK	P02965 bacillus th
8	2496.5	57.3	1181	1 C1AE_BACTL	Q03748 bacillus th
9	2477	56.8	1179	1 C1AD_BACTA	Q03744 bacillus th
10	2449	56.2	1170	1 C1JB_BACTU	Q45716 bacillus th
11	2374.5	54.5	1155	1 C1AB_BACTK	P06578 bacillus th
12	2372.5	54.4	1174	1 C1EB_BACTA	Q03745 bacillus th
13	2367.5	54.3	1174	1 C1FA_BACTU	Q03746 bacillus th
14	2364.5	54.3	1176	1 C1AG_BACTU	Q08515 bacillus th
15	2354	54.0	1169	1 C1FB_BACTM	Q66377 bacillus th
16	2352	54.0	1169	1 C1GB_BACTZ	Q92426 bacillus th
17	2334.5	53.6	1178	1 C1AC_BACTK	P05068 bacillus th
18	2287.5	52.5	1166	1 C1CA_BACTU	Q45746 bacillus th
19	2281	52.3	1155	1 C1HB_BACTM	Q45718 bacillus th
20	2221	51.0	1172	1 C1HA_BACTU	Q45748 bacillus th
21	2018	46.3	911	1 C1AF_BACTU	P96315 bacillus th
22	1980	45.4	1228	1 C1BA_BACTK	P05517 bacillus th
23	1965.5	45.1	1229	1 C1BB_BACTU	Q45739 bacillus th
24	1944.5	44.6	1233	1 C1BC_BACTM	Q45774 bacillus th
25	1940.5	44.5	1215	1 C1CA_BACTM	Q45715 bacillus th
26	1869.5	42.9	1227	1 C1BE_BACTU	O85805 bacillus th
27	1836.5	42.1	1231	1 C1BD_BACTZ	Q92425 bacillus th
28	1690	38.8	1138	1 C7AB_BACTU	Q45708 bacillus th
29	1674	38.4	1138	1 C7AB_BACTA	Q45707 bacillus th
30	1609	36.9	1138	1 C7AA_BACTU	Q03749 bacillus th
31	1490	34.2	1169	1 C8BA_BACTU	Q45705 bacillus th
32	1403	32.2	1163	1 CQAA_BACTP	Q9X597 bacillus th
33	1396	32.0	1157	1 C8AA_BACTU	Q45704 bacillus th

ALIGNMENTS

RESULT 1

ID	CICA_BACTE	STANDARD;	PRT;	1189 AA.
AC	P05518; P10327; Q03742; Q45725;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	30-MAY-2000 (Rel. 35, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pesticidal crystal protein cryIcA (insecticidal delta-endotoxin			
DE	CRYIC(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).			
GN	CRYICA OR CRYIC(A) OR CRYIC.			
OS	Bacillus thuringiensis (subsp. entomocidus), and			
OS	Bacillus thuringiensis (subsp. aizawai).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1436, 1433;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=B.t. entomocidus; STRAIN=60.5;			
RX	MEDLINE=88289380; PubMed=3399402;			
RA	Honee G.; van der Salm T.P.M.; Visser B.;			
RT	"Nucleotide sequence of crystal protein gene isolated from B.			
RT	thuringiensis subspecies entomocidus 60.5 coding for a toxin highly			
RT	active against Spodoptera species."			
RL	Nucleic Acids Res. 16:6240-6240(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=B.t. aizawai; STRAIN=NRRL B-19484 / PS811;			
RX	Payne J.M.; Sick A.J.;			
RA	"Bacillus thuringiensis isolate active against lepidopteran pests, and			
RT	genes encoding novel lepidopteran-active toxins."			
RL	Patent number US5246852, 21-SEP-1993.			
RN	[3]			
RP	SEQUENCE OF 1-823 FROM N.A.			
RC	SPECIES=B.t. aizawai; STRAIN=7-29;			
RX	MEDLINE=89343627; PubMed=2548060;			
RA	Sanchis V.; Lerechus D.; Menou M.; Chauvaux J.; Guo S.; Lecadet M.-M.;			
RT	"Nucleotide sequence and analysis of the N-terminal coding region of			
RT	the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis			
RL	aizawai 7.29."			
RN	[4]			
RP	SEQUENCE OF 1-756 FROM N.A.			
RC	SPECIES=B.t. aizawai; STRAIN=7-29 / K26-21;			
RA	Strizhov N.;			
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT			
CC	EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTEA			
CC	SPECIES.			
CC	-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING			
CC	SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART			
CC	OF THE SPORE COAT.			
CC	-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE			
CC	N-TERMINUS.			
CC	-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			

Q45733 bacillus th
Q45709 bacillus th
Q45752 bacillus th
O06014 bacillus th
Q9xdl1 bacillus th
O87404 bacillus th
Q9xnl9 bacillus th
Q45706 bacillus th
Q99031 bacillus th
Q9x682 bacillus th
P17969 bacillus th
P07130 bacillus th

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CC -----
 CC EMBL; X07518; CAA30396.1; -
 CC EMBL; M73251; AAA22343.1; -
 CC EMBL; X13620; CAA31951.1; -
 CC EMBL; X96682; CAA65457.1; -
 CC PIR; S00944; S00944.
 CC PIR; S04181; S04181.
 CC HSP; P02965; IC1Y.
 CC InterPro; IPR001178; Endotoxin.
 CC InterPro; IPR005638; endotoxin_C.
 CC InterPro; IPR005639; endotoxin_N.
 CC Pfam; PF00555; endotoxin_1.
 CC Pfam; PF03944; endotoxin_C; 1.
 CC Pfam; PF03945; endotoxin_N; 1.
 CC Toxin; Sporulation.
 CC CONFLICT 124 124 A -> B (IN REF. 1).
 CC CONFLICT 294 244 A -> R (IN REF. 1).
 CC CONFLICT 366 366 N -> I (IN REF. 3).
 CC CONFLICT 376 380 WPAP -> CORRH (IN REF. 3).
 CC CONFLICT 386 386 V -> G (IN REF. 3).
 CC CONFLICT 405 405 T -> Q (IN REF. 2).
 CC CONFLICT 453 453 H -> A (IN REF. 1).
 CC CONFLICT 775 775 R -> D (IN REF. 3).
 CC CONFLICT 853 853 V -> L (IN REF. 2).
 CC CONFLICT 864 864 G -> N (IN REF. 2).
 CC CONFLICT 931 931 D -> N (IN REF. 2).
 CC SEQUENCE 1189 AA; 134715 MW; 362768685916A0DF CRC64;

Query Match 98.5%; Score 4294; DB 1; Length 1189;
 Best Local Similarity 99.0%; Pred. No. 1.5e-296;
 Matches 815; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNNQICPNCLNPEEVLIDGERISTGSSIDISLVQPLVNSFVPGGFLVGLI 60
 DB 1 MEENNNQICPNCLNPEEVLIDGERISTGSSIDISLVQPLVNSFVPGGFLVGLI 60
 QY 61 DFVWGVGSQWDAFLVQIEQLINERITAFARNAANLEGLNENNIYVEAFKEWEDP 120
 DB 61 DFVWGVGSQWDAFLVQIEQLINERITAFARNAANLEGLNENNIYVEAFKEWEDP 120
 QY 121 NNATRTVIDRILDGLERDIPSRISGFEVPLSVYAAQANLHLIRDSVIFGER 180
 DB 121 NNATRTVIDRILDGLERDIPSRISGFEVPLSVYAAQANLHLIRDSVIFGER 180
 QY 181 WGLTTINVENNRLIRHIDYADHCANTYNNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
 DB 181 WGLTTINVENNRLIRHIDYADHCANTYNNRGLNLPKSTYQDWITYNRLRDLTLTVL 240
 QY 241 DIAAFFPNYDNRYPQVGLTREVTYDPLINPNQVLAQPTFNVMSSAIRNPHL 300
 DB 241 DIAAFFPNYDNRYPQVGLTREVTYDPLINPNQVLAQPTFNVMSSAIRNPHL 300
 QY 301 FDILNLTITDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQBPSPFTFNGPV 360
 DB 301 FDILNLTITDWFVSGRNFYWGHRVVISLIGGNITSPYIGREANQBPSPFTFNGPV 360
 QY 361 FRTLSTPTLRLLQCPQORHFNLRGEGVEFTPTNSFTYGRGTVDLSLTLPEDNSVP 420
 DB 361 FRTLSTPTLRLLQCPQORHFNLRGEGVEFTPTNSFTYGRGTVDLSLTLPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPTLTGTVFWSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
 DB 421 PREGYSHRLCHATFVQSGTPTLTGTVFWSWTHRSATLNTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGFTGGDILRENTFGDVFSLQVNNINSPTQRYRLFRFYASSRDARVILTGAA 540
 DB 481 GTSVITGPGFTGGDILRENTFGDVFSLQVNNINSPTQRYRLFRFYASSRDARVILTGAA 540

QY 541 STVGGOVSNVPLQKTMETIGENITSTRYTDYDFNSFPNPNPDIIGISEQPLFGAGSI 600
 DB 541 STVGGOVSNVPLQKTMETIGENITSTRYTDYDFNSFPNPNPDIIGISEQPLFGAGSI 600
 QY 601 SSSELXIDKIEIILADATFAESDLERAQKAVNALFTSSNQIGLKTVDYDHYDQVSNLV 660
 DB 601 SSSELXIDKIEIILADATFAESDLERAQKAVNALFTSSNQIGLKTVDYDHYDQVSNLV 660
 QY 661 DCLSDPEFLDKRELSEKVKHAKRLSDERNLLQDNPFRGINRQPDRCWRGSTDITIQGSD 720
 DB 661 DCLSDPEFLDKRELSEKVKHAKRLSDERNLLQDNPFRGINRQPDRCWRGSTDITIQGSD 720
 QY 721 DVFKENYVTLPGTVDECYPTVLYQKIDESKLKAYTRYLRCYIEDSDLEIYLIAVNAKH 780
 DB 721 DVFKENYVTLPGTVDECYPTVLYQKIDESKLKAYTRYLRCYIEDSDLEIYLIAVNAKH 780
 QY 781 EIVNVPTGSLWPLSAQSPICKGEPNRCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPTGSLWPLSAQSPICKGEPNRCAPHLEWNPDLDCSC 823

RESULT 2

C1CB_BACTG ID C1CB_BACTG STANDARD; PRT; 1176 AA.
 AC P56953; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIcB (Insecticidal delta-endotoxin
 DE CryIc(b)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
 GN CRYI3C OR CRYI3C(B).
 OS Bacillus thuringiensis (subsp. galleriae).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI TaxID:29338;
 RN [1] TaxID:29338;
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD-29;
 RC MEDLINE=93236401; PubMed=8476286;
 RA Kalman S.S.;
 RT "Cloning a novel cryIc-type gene from a strain of Bacillus
 RT thuringiensis galleriae".
 RL Appl. Environ. Microbiol. 59:1131-1137(1993).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS. TOXIC TO SPODOPTERA EXIGUA AND
 CC TRICHLUSIA N.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOGULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; M97880; -; NOT_ANNOTATED_CDS.
 CC PIR; A48970; A48970.
 CC HSP; P02965; IC1Y.
 CC InterPro; IPR001178; Endotoxin.
 CC InterPro; IPR005638; endotoxin_C.
 CC InterPro; IPR005639; endotoxin_N.
 CC Pfam; PF00555; endotoxin_1.
 CC Pfam; PF03944; endotoxin_C; 1.
 CC Pfam; PF03945; endotoxin_N; 1.
 CC Toxin; Sporulation.
 CC SEQUENCE 1176 AA; 132867 MW; 108233494C2AC018 CRC64;

Query Match

80.2%; Score 3495.5; DB 1; Length 1176;

Best Local Similarity 80.7%; Pred. No. 7.1e-240;
Matches 668; Conservative 48; Mismatches 89; Indels 23; Gaps 4;

QY 1 MEENNOQCPYNCLSNPEVLDDGRISTGSSIDISLSVQLVSNFVPGGFLVGLI 60
DB 1 MENNIQOQVFNCLSNPEILLDGRISTGSSIDISLSVQLVSNFVPGGFLVGLI 60

QY 61 DFWMGIVGSPQDAFLVQIEQLINERIAEFARNAATANLEGNNFNIIYVEAFKEWEDP 120
DB 61 DFWMGIVGSPQDAFLVQIEQLINERIAEFARNAATANLEGNNFNIIYVEAFKEWEDP 120

QY 121 NNPAETRVDRPRILLDGLERDIPSFRIISGVEPLLSVYAQAANHLAILRDSVIFGR 180
DB 121 DNPVTRVDRPRILLDGLERDIPSFRIISGVEPLLSVYAQAANHLAILRDSVIFGR 180

QY 181 WGLTINNVNENYRLIRHIDEYADHCANTYNNGLNLPKSTYQDWITYNRLRDLTLVL 240
DB 181 WGLTINNVNENYRLIRHIDEYADHCANTYNNGLNLPKSTYQDWITYNRLRDLTLVL 240

QY 241 DIAAPPNDYRRYPQVQQLTREYVTDPLINFPQLOSVAQLPTFNVMSSAIRNPHL 300
DB 241 DIAAPPNDYRRYPQVQQLTREYVTDPLINFPQLOSVAQLPTFNVMSSAIRNPHL 300

QY 301 FDLANLTIPTDWFSGRNPYWGHRVVISLGGNITSPYIGREANQPPRSFTFNGPV 360
DB 301 FDLANLTIPTDWFSGRNPYWGHRVVISLGGNITSPYIGREANQPPRSFTFNGPV 360

QY 361 FRTLSTPTLRLQPCORHFNLRGGEVEFTPTNSFTYRGRTVDSLTLPEDNSVP 420
DB 361 FRTLSTPTLRLQPCORHFNLRGGEVEFTPTNSFTYRGRTVDSLTLPEDNSVP 420

QY 421 PREGYSHRLCHATFVQSGTPELTGVPFVSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
DB 421 PREGYSHRLCHATFVQSGTPELTGVPFVSWTHRSATLNTIDPERINQIPLVKGFRVMG 480

QY 481 GTSVITGPGFTGDIILRTFGDFVSLQVNSPITQRLRFRVASSRDARVILTGAA 540
DB 481 GTSVITGPGFTGDIILRTFGDFVSLQVNSPITQRLRFRVASSRDARVILTGAA 540

QY 541 STGVGGQVSNVPLQKTEIGENLSTRTRYTDFSNPPFRANPDIGISEQLPFCAG-S 599
DB 541 STGVGGQVSNVPLQKTEIGENLSTRTRYTDFSNPPFRANPDIGISEQLPFCAG-S 599

QY 599 SVTVGGSTTGNQGFSTMSANGALTSQSFRFAEP-----VGLSASGQASIS 582
DB 599 SVTVGGSTTGNQGFSTMSANGALTSQSFRFAEP-----VGLSASGQASIS 582

QY 600 ISSG-----ELYIKIEIILADATPEASDLERAQAVNALFTSSNQIGLKTVDYHIDQ 655
DB 600 ISSG-----ELYIKIEIILADATPEASDLERAQAVNALFTSSNQIGLKTVDYHIDQ 655

QY 655 VSNLVDCLSDERCLDEKRELSKVHAKLSDERNLQDPNFRGNGRQDGRWGSTDIT 715
DB 655 VSNLVDCLSDERCLDEKRELSKVHAKLSDERNLQDPNFRGNGRQDGRWGSTDIT 715

QY 715 IOGGDDVPKENYVTLPGTVDECVPTLYOKIDESKIKAYTRYELRGYIEDSDLEIYLIA 775
DB 715 IOGGDDVPKENYVTLPGTVDECVPTLYOKIDESKIKAYTRYELRGYIEDSDLEIYLIA 775

QY 775 YNAKHEIVNVPGTGSILWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
DB 775 YNAKHEIVNVPGTGSILWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823

QY 823 YNAKHEIVNVPGTGSILWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 810
DB 823 YNAKHEIVNVPGTGSILWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 810

RESULT 3
ID C1EA BACTX
AC Q57458; Q03741;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cryIEa (Insecticidal delta-endotoxin
DE CryIE(a) (CryIE(a) entomocidal protoxin) (133 kDa crystal protein).
GN CRYIEA OR CRYIE(A) OR CRYIC(B) OR BTXI OR BTL1.
OS Bacillus thuringiensis (subsp. kenya).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=33930;

Sequence from N.A.
MEDLINE=91081338; PubMed=2259636;
Bosse M., Masson L., Brousseau R.;
"Nucleotide sequence of a novel crystal protein gene isolated from
Bacillus thuringiensis subsp. kenya";
Nucleic Acids Res. 18:7443-7443(1990).
Sequence from N.A.
STRAIN=4F1;
MEDLINE=91072224; PubMed=2254254;
Visser B., Munsterman E., Stoker A., Dirkse W.G.;
"A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-
specific crystal protein";
J. Bacteriol. 172:6783-6788(1990).
Sequence from N.A.
STRAIN=PSB1F;
Payne J.M., Sick A.J.;
"Novel Bacillus thuringiensis isolate denoted B.t. PSB1F, active
against lepidopteran pests, and a gene encoding a lepidopteran-active
toxin";
Patent number US039523, 13-AUG-1991.
-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTERA
SPECIES.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
-!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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EMBL; X56144; CAA39609.1; -;
EMBL; X53985; CAA37933.1; -;
EMBL; M73252; AAA22345.1; -;
PIR; I40572; I40572.
HSP; P02965; 1CIY.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
Pfam; PF03944; endotoxin_1.
Pfam; PF03945; endotoxin_N; 1.
Toxin; Sporulation.
FT CONFLICT 862 862 N -> K (IN REF. 3).
SQ SEQUENCE 1171 AA; 133252 MW; 5758FB5ABDBSABE CRC64;
Query Match 61.5%; Score 2680; DB 1; Length 1171;
Best Local Similarity 64.5%; Pred. No. 5.3e-182;
Matches 536; Conservative 88; Mismatches 169; Indels 38; Gaps 15;

QY 4 NNQNCIPYCNCLSNPEVLDDGRISTGSSIDISLSL-VQFLVSNFVPGGFLVGLIDF 62
DB 4 NNQNCIPYCNCLSNPEVLDDGRISTGSSIDISLSL-VQFLVSNFVPGGFLVGLIDF 62

QY 5 NNQNCIPYCNCLSNPEVLDDGRISTGSSIDISLSL-VQFLVSNFVPGGFLVGLIDF 61
DB 5 NNQNCIPYCNCLSNPEVLDDGRISTGSSIDISLSL-VQFLVSNFVPGGFLVGLIDF 61

QY 63 VVGIVGSPQDAFLVQIEQLINERIAEFARNAATANLEGNNFNIIYVEAFKEWEDPN 122
DB 63 VVGIVGSPQDAFLVQIEQLINERIAEFARNAATANLEGNNFNIIYVEAFKEWEDPN 122

QY 62 IWGIGSPQDAFLVQIEQLINERIAEFARNAATANLEGNNFNIIYVEAFKEWEDPN 121
DB 62 IWGIGSPQDAFLVQIEQLINERIAEFARNAATANLEGNNFNIIYVEAFKEWEDPN 121

QY 123 PATRTRVDRPRILLDGLERDIPSFRIISGVEPLLSVYAQAANHLAILRDSVIFGR 182
DB 123 PATRTRVDRPRILLDGLERDIPSFRIISGVEPLLSVYAQAANHLAILRDSVIFGR 182

QY 122 PALKEEMTQFDNMSILVTAIPULFSVQNYQVPLSVYAQAANHLAILRDSVIFGR 181
DB 122 PALKEEMTQFDNMSILVTAIPULFSVQNYQVPLSVYAQAANHLAILRDSVIFGR 181

QY 183 LTTINNVNENYRLIRHIDEYADHCANTYNNGLNLPKSTYQDWITYNRLRDLTLVL 241
DB 183 LTTINNVNENYRLIRHIDEYADHCANTYNNGLNLPKSTYQDWITYNRLRDLTLVL 241

Db 182 FDIATNSRYNDLTRELIPIYDYAVRWYNTGLDRPRTGGLRNWARFNQFRRELTISVLD 241
 Qy 242 IAAFFPNYONRYPTQPVGQLTREVYDPLINFPQLOSAQVAFPTFNVMESAIKRNPHLF 301
 Db 242 IISFFRYSRLYPIPTSSQLTREVYDPLINFPQLOSAQVAFPTFNVMESAIKRNPHLF 297
 Qy 302 DILNNLTFTDWFSGVGRNFMGHRVSSLLIGGN-ITSPYIGREANQPPPSF---TFN 357
 Db 298 DFLNNLTFTD--LIRGVHYWAGHRVTSHTSGSSQVITTPQYGTANASPRRTIAPSTFP 355
 Qy 358 G--PVFETLSIPTLRLLQPCORHNNLRGGEVFSPTNS-FTVRGRTGVDSTLLEPP 414
 Db 356 GLNLFYKTLNPPFRSENITPTLGINV--VQGVGFIQPNNAEVLVRSRGTVDLSNELPI 413
 Qy 415 E-DNSVPPREGYSHRLCHATFVQSGTPELTGTVGVFSWTHRSATLNTIDPERINOIPLV 473
 Db 414 DGENSL---VGYSHRLSHVTLTRSLYNTNITSLPTFVTHHSATNTINPDIIQIPLV 470
 Qy 474 KGRVWGGTSVITGPGFTGGDILRRNTPGDFVSLQVNSPITQRYLRFVASSRDARV 533
 Db 471 KGRVWGGTSVITGPGFTGGDILRRNTPGDFVSLQVNSPITQRYLRFVASSRDARV 530
 Qy 534 IYLVGAASGCGVQSVNMPLOKTMETIGENLTSRFTYDTSNPFSPFRANPDIIIGISEQ- 592
 Db 531 TV-----AIGQIRVDMTLEKTMETIGESLTSRFTYDTSNPFSPFRANPDIIIGISEQ 583
 Qy 593 PLFGAGSISSELYIDKIEIILADATFEASDLERAQKAVNALFTSNQIGLKTVDITYH 652
 Db 584 PIRG-----GELYIDKIEIILADATFEASDLERAQKAVNALFTSNQIGLKTVDITYH 637
 Qy 653 IDQVSNLVDCLSDFCLDEKRELSKVKAKRLSDERNLLQDPNFRGNRQPDGRWGST 712
 Db 638 IDQVSNLVDCLSDFCLDEKRELSKVKAKRLSDERNLLQDPNFRGNRQPDGRWGST 697
 Qy 713 DITIQGGDDVFNKENVYTLPGTVDCYPTLYQKIDESKLYATRYELRGVIEDSDLEIY 772
 Db 698 DITIQGGDDVFNKENVYTLPGTVDCYPTLYQKIDESKLYATRYELRGVIEDSDLEIY 757
 Qy 773 LIYANAKHETVNVPGTSLMPLSAQSPGKCGPNRCAHLEWNPDLDCSC 823
 Db 758 LIYANAKHETVNVPGTSLMPLSAQSPGKCGPNRCAHLEWNPDLDCSC 808

RESULT 4

ID CLDB_BACTU STANDARD; PRT; 1160 AA.
 AC Q45747;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIb (insecticidal delta-endotoxin
 DE CryID(b)) (Crystalline entomocidal protoxin) (131 kDa crystal protein).
 GN BACILLUS THURINGIENSIS.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1428;
 OX 1;
 RN SEQUENCE FROM N.A.
 RP STRAIN=BTS0349A;
 RC Lambert B.;
 RA Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORE FORMATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)

CC -----
 CC EMBL; Z22511; CAA80234.1; -
 CC PIR; S32647; S32647.
 CC HSSP; P02965; 1CIY.
 CC InterPro; IPR001178; Endotoxin.
 CC InterPro; IPR005638; endotoxin_C.
 CC InterPro; IPR005639; endotoxin_N.
 CC Pfam; PF00555; endotoxin_1.
 CC Pfam; PF03944; endotoxin_C.
 CC Pfam; PF03945; endotoxin_N.
 CC Toxin; Sporulation.
 CC KW
 CC SQ SEQUENCE 1160 AA; 130968 MW; B18B18748B40695E CRC64;

Query Match 59.3%; Score 2584; DB 1; Length 1160;
 Best Local Similarity 61.9%; Pred No 3 4e-175;
 Matches 513; Conservative 80; Mismatches 200; Indels 36; Gaps 12;

Qy 1 MEENQNCIPYCNLSNDEEVLIDGERISGTGSSDIDSLVQFLVSNFVGGGLVGLI 60
 Db 1 MDINHQCIPYCNLSNDEEVLIDGERISGTGSSDIDSLVQFLVSNFVGGGLVGLI 60
 Qy 61 DFVWGVGSQWDAFLVQIEQLINERIAEPANNAIANLEGLGNFNVIYEAKEWEDP 120
 Db 61 ELIWMGFVGSQWDAFLVQIEQLINERIAEPANNAIANLEGLGNFNVIYETFAWEKDP 120
 Qy 121 NNPAITRVIDFRILDGLLEROIPIPSRISGFEVPLSVYAAQANLHAILRDSVIFGER 180
 Db 121 SNPALREEMKTOFNVMNSALIAIPLLRVRYNEVALLSVYVQAANLHSLRDSVYQOR 180
 Qy 181 WGLTNTNVENTNRLIRHIDEYADHCANTYNGLNLPKSTYQDWITNRLRDLTLTVL 240
 Db 181 WGPDPATVNSRYSDLTRLHVYTDHCVDTYNDGLNLEGRSLSDVWVYRFRRLTISVL 240
 Qy 241 DIAAFPNDNRRYPIQVQGLTREVYD--PLINFNPLQSAQVLPFTFNVMESAIKRNPH 299
 Db 241 DIAAFPNDYIEAPYIQTASQLTREVYDLPFV--NETLSPASYPYTFSAESAIAIRSPH 298
 Qy 300 LFDILNNLTFTDWFSGVGRNFMGHRVSSLLIGGN--ITSPYIGREANQPPPSFTFN 357
 Db 299 LVDELNSFTIYD--SLASYAYWGGHLVNSFRTGTTNLRSLPYGREGNTERPVTISAS 356
 Qy 358 G--PVFETLSIPTLRLLQPCORHNNLRGGEVFSPTNSFTYRGRGTVDSLTELPE 415
 Db 357 PSVDFETLSYFTGLNPNP-----VAGIEGVFQNTISRSYRKSGLDSELPQP 409
 Qy 416 DNSYPRREGYSHRLCHATFVQSGTPELTGTVGVFSWTHRSATLNTIDPERINOIPLVKG 475
 Db 410 DVSVPALGVSHRLCHATFLEISGPRI-AGIVFWSWTHRSASPIVSPRITQIPWKA 468
 Qy 476 FRVWGGTSVITGPGFTGGDILRRNTPGDFVSLQVNSPITQRYLRFVASSRDARVIV 535
 Db 469 HTLASGASVYKPGFTGGDILRRNTPGDFVSLQVNSPITQRYLRFVASSRDARVIV 521
 Qy 536 LTGAASGCGVQSVNMPLOKTMETIGENLTSRFTYDTSNPFSPFRANPDIIIGISEQL 594
 Db 522 ANRSGTFRYSQPPSYGVSFPKTMADGALTSRFAHTLFTPTIFSRQA-----EEDFL 575
 Qy 595 FGAISISSGELYIDKIEIILADATFEASDLERAQKAVNALFTSNQIGLKTVDITYHID 654
 Db 576 Y----IQSG-VYIDRIEFIPVDATFESEINLERAKAVNALFTSNQIGLKTVDITYHID 630
 Qy 655 QVSNLVDCLSDFCLDEKRELSKVKAKRLSDERNLLQDPNFRGNRQPDGRWGSTDI 714
 Db 631 QVSNLVDCLSDFCLDEKRELSKVKAKRLSDERNLLQDPNFRGNRQPDGRWGSTDI 690
 Qy 715 TIQGGDDVFNKENVYTLPGTVDCYPTLYQKIDESKLYATRYELRGVIEDSDLEIYLI 774
 Db 691 TIQGGDDVFNKENVYTLPGTVDCYPTLYQKIDESKLYATRYELRGVIEDSDLEIYLI 750

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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:20:48 ; Search time 45 Seconds
(without alignments)
1758.818 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNQOCIPYNCLSNPDEE.....GEPNRCAPHLEWNPDLDCSC 823
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4358	100.0	823	2 S04181	parasporal crystal
2	4275	98.1	823	2 S00944	parasporal crystal
3	3495.5	80.2	1176	2 A48970	parasporal crystal
4	3374	77.4	655	2 JC7140	protoxin - Bacillu
5	2680	61.5	1171	2 A37829	parasporal crystal
6	2680	61.5	1171	2 I40572	parasporal crystal
7	2584	59.3	1160	2 S32647	parasporal crystal
8	2573	59.0	1165	2 S11446	parasporal crystal
9	2531.5	58.1	1176	2 JT0241	parasporal crystal
10	2530.5	58.1	934	2 A22798	parasporal crystal
11	2525.5	58.0	1176	2 JC2219	parasporal crystal
12	2518.5	57.8	1176	2 A22617	parasporal crystal
13	2518.5	57.8	1176	2 S02215	parasporal crystal
14	2496.5	57.3	1181	2 A41052	parasporal crystal
15	2378.5	54.6	1155	2 A26513	parasporal crystal
16	2374.5	54.5	1155	2 JD0002	parasporal crystal
17	2374.5	54.5	1156	2 A29125	parasporal crystal
18	2367.5	54.3	1174	2 A42459	parasporal crystal
19	2363.5	54.2	1155	2 S02134	parasporal crystal
20	2363.5	54.2	1155	2 I39838	parasporal crystal
21	2355	54.0	1174	2 S32649	parasporal crystal
22	2334.5	53.6	1178	1 USRSXH	parasporal crystal
23	2332	53.5	1177	2 A49785	parasporal crystal
24	2287.5	52.5	1166	2 S32645	parasporal crystal
25	2247	51.6	1156	2 A29838	parasporal crystal
26	2221	51.0	1172	2 S32689	parasporal crystal
27	1980	45.4	1228	2 S00873	parasporal crystal
28	1509	36.9	1138	2 A48944	parasporal crystal
29	1381	31.7	1157	1 S49247	parasporal crystal

30	1354	31.1	618	2 S11445	parasporal crystal
31	1340.5	30.8	719	2 I40590	cryv465 protein -
32	1331.5	30.6	719	2 I39815	insecticidal prote
33	1326	30.4	1154	2 S39536	parasporal crystal
34	1322.5	30.3	719	2 S25383	parasporal crystal
35	1316.5	30.2	719	2 I39814	insecticidal prote
36	1125.5	25.8	1160	2 I40589	parasporal crystal
37	1042.5	23.9	1156	2 S19306	parasporal crystal
38	921.5	21.1	659	2 S10228	parasporal crystal
39	912.5	20.9	652	2 A27323	parasporal crystal
40	907.5	20.8	652	2 I39811	parasporal crystal
41	899	20.6	1136	1 USBS81	parasporal crystal
42	847.5	19.4	934	2 B29838	parasporal crystal
43	839	19.3	1180	2 A26858	parasporal crystal
44	838	19.2	1180	2 I39870	parasporal crystal
45	811.5	18.6	649	1 JH0261	parasporal crystal

ALIGNMENTS

RESULT 1

S04181
parasporal crystal protein - Bacillus thuringiensis (strain aizawai 7.29) (fragment)
N/Alternate names: delta-endotoxin
C/Species: Bacillus thuringiensis
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C/Accession: S04181
R/Sanchis, V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.; Lecadet, M.M.
Mol. Microbiol. 3, 229-238, 1989
A/Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda delta-endotoxin
A/Reference number: S04181; MUID:89343627; PMID:2548060
A/Accession: S04181
A/Molecule type: DNA
A/Residues: 1-823 <S>
A/Cross-references: EMBL:X13620; NID:g40355; PIDN:CAA31951.1; PID:g40356
C/Genetics:
A/Gene: bta
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match	100.0%	Score	4358	DB 2	Length	823			
Best Local Similarity	100.0%	Pred.	3.3e-307						
Matches	823	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Y	1	MEENNQOCIPNCLSNPEEVLDDGERISTGNSSTIDISLSLVQFLVSNFVPGGFLVGLI	60						
b	1	MEENNQOCIPNCLSNPEEVLDDGERISTGNSSTIDISLSLVQFLVSNFVPGGFLVGLI	60						
Y	61	DFVMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGIGNNFNIYVEAFKEWSDP	120						
b	61	DFVMGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGIGNNFNIYVEAFKEWSDP	120						
Y	121	NNPATRTRVIDRFRILDLGLERDIPSPRISGFEVPLLSVYAQAANLHAILRDSVIGER	180						
b	121	NNPATRTRVIDRFRILDLGLERDIPSPRISGFEVPLLSVYAQAANLHAILRDSVIGER	180						
Y	181	WGLTTINVENNRYLIRHIDYADHCANTYRGNLNLKSTVDWITYNRLRDLTLTVL	240						
b	181	WGLTTINVENNRYLIRHIDYADHCANTYRGNLNLKSTVDWITYNRLRDLTLTVL	240						
Y	241	DIAAFPNYDNRYPPIQPVGQLTREYVTDPLINFPQLQSVQALPTFNVMESSAIRNPHL	300						
b	241	DIAAFPNYDNRYPPIQPVGQLTREYVTDPLINFPQLQSVQALPTFNVMESSAIRNPHL	300						
Y	301	FDILNNLTFTDWSVGRNFWGGRHVRVTSIIIGGNITSPYIGREANQEPFRSFTFNGVP	360						
b	301	FDILNNLTFTDWSVGRNFWGGRHVRVTSIIIGGNITSPYIGREANQEPFRSFTFNGVP	360						
Y	361	FRTLSIPTLRLLQPCQRHHNLRGCGVEESTPTNSFTYGRGTVDSLTELPPEDNSVP	420						
b	361	FRTLSIPTLRLLQPCQRHHNLRGCGVEESTPTNSFTYGRGTVDSLTELPPEDNSVP	420						

421 PREGYSHRLCHATFVQSGTTPPLTTCGVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
421 PREGYSHRLCHATFVQSGTTPPLTTCGVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPIRTORYLRFRYASSRDARVILVTGAA 540
481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPIRTORYLRFRYASSRDARVILVTGAA 540
541 STVGGOVSNMPLQKTMKEIGENLTSTRTYTDPSNPPSFRANPDIIIGISQPLFGAGSI 600
541 STVGGOVSNMPLQKTMKEIGENLTSTRTYTDPSNPPSFRANPDIIIGISQPLFGAGSI 600
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTHIDQVSNLV 660
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTHIDQVSNLV 660
661 DCLSDFECLDKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720
661 DCLSDFECLDKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
781 EIVNVPGTGSMLPWSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
781 EIVNVPGTGSMLPWSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 2

S00944
parasporal crystal protein crylCal - Bacillus thuringiensis (strain entomocidus 60.5)
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
C:Accession: S00944
R:Honee, G.; van der Salm, T.; Visser, B.
Nucleic Acids Res. 16, 6240, 1988
A:Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subsp.
A:Reference number: S00944; MUID:88289380; PMID:3359402
A:Accession: S00944
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1189 <HON>
A:Cross-references: EMBL:X07518; NID:940293; PIDN:CAA30396.1; PID:940294
A:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 98.1%; Score 4275; DB 2; Length 1189;
Best Local Similarity 98.7%; Pred. No. 6.2e-301;
Matches 812; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEENNONCIPYNCNLSNPEEVLDDGERISTGNSSIDISLVQFLVSNFVPGGGFLVGLI 60
DB 1 MEENNONCIPYNCNLSNPEEVLDDGERISTGNSSIDISLVQFLVSNFVPGGGFLVGLI 60
QY 61 DFWMGIVGPSQWDAFLVQIEQLINERIAFAFARNAAIANLEGLGNFNFIYVEAFKEWEEDP 120
DB 61 DFWMGIVGPSQWDAFLVQIEQLINERIAFAFARNAAIANLEGLGNFNFIYVEAFKEWEEDP 120
QY 121 NNPATRTRVIDRFRILDGLLERDIPSFRISSGFVEPLLSVYAAANLHAILRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSFRISSGFVEPLLSVYAAANLHAILRDSVIFGER 180
QY 181 WGLTITNVNENYRLIRHIDEYADHCANTYNRGLNLPKSTYQDMITTYNRLRDLTLTVL 240
DB 181 WGLTITNVNENYRLIRHIDEYADHCANTYNRGLNLPKSTYQDMITTYNRLRDLTLTVL 240
QY 241 DIAAPFNVDNRRYPIQVQGLTRVYTDPLNFNPQLQSVQALPTFNWMSAIRPHL 300
DB 241 DIAAPFNVDNRRYPIQVQGLTRVYTDPLNFNPQLQSVQALPTFNWMSAIRPHL 300
QY 301 FDIANLITFTDPSVGVNFWGCHRVISLIGGNTSPICYREANQPPRSFTFNGPV 360

301 FDIANLITFTDPSVGVNFWGCHRVISLIGGNTSPICYREANQPPRSFTFNGPV 360
361 FRTLSIPTLRLLQOPQORHFNLRGEGVEFSFTPTNSFTYRGRGTVDSLTLPEDNSVP 420
361 FRTLSIPTLRLLQOPQORHFNLRGEGVEFSFTPTNSFTYRGRGTVDSLTLPEDNSVP 420
421 PREGYSHRLCHATFVQSGTTPPLTTCGVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
421 PREGYSHRLCHATFVQSGTTPPLTTCGVFVSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPIRTORYLRFRYASSRDARVILVTGAA 540
481 GTSVITGPGTGGDILRNTFGDFVSLQVNSPIRTORYLRFRYASSRDARVILVTGAA 540
541 STVGGOVSNMPLQKTMKEIGENLTSTRTYTDPSNPPSFRANPDIIIGISQPLFGAGSI 600
541 STVGGOVSNMPLQKTMKEIGENLTSTRTYTDPSNPPSFRANPDIIIGISQPLFGAGSI 600
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTHIDQVSNLV 660
601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTHIDQVSNLV 660
661 DCLSDFECLDKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720
661 DCLSDFECLDKRELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTITIOGGD 720
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
721 DVFKNYVTLPGTVDECPYLYQKIDSKLKAYTRYELRGYIEDSDLEIYLIAYNAXH 780
781 EIVNVPGTGSMLPWSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
781 EIVNVPGTGSMLPWSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 3

A48970
parasporal crystal protein crylCb - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C:Accession: A48970
R:Kelman, S.; Kiehne, K.L.; Libs, J.L.; Yanamoto, T.
Appl. Environ. Microbiol. 59, 1131-1137, 1993
A:Title: Cloning of a novel cryIC-type gene from a strain of Bacillus thuringiensis subsp.
A:Reference number: A48970; MUID:93236401; PMID:8476286
A:Accession: A48970
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-1176 <KAL>
A:Cross-references: GB:M97880; NID:9289263
A:Experimental source: subsp. Gallieriae HD29
A:Note: sequence extracted from NCBI backbone (NCBIN:129672, NCBIP:129675)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 80.2%; Score 3495.5; DB 2; Length 1176;
Best Local Similarity 80.7%; Pred. No. 1.8e-244;
Matches 668; Conservative 48; Mismatches 89; Indels 23; Gaps 4;

QY 1 MEENNONCIPYNCNLSNPEEVLDDGERISTGNSSIDISLVQFLVSNFVPGGGFLVGLI 60
DB 1 MEENNONCIPYNCNLSNPEEVLDDGERISTGNSSIDISLVQFLVSNFVPGGGFLVGLI 60
QY 61 DFWMGIVGPSQWDAFLVQIEQLINERIAFAFARNAAIANLEGLGNFNFIYVEAFKEWEEDP 120
DB 61 DFWMGIVGPSQWDAFLVQIEQLINERIAFAFARNAAIANLEGLGNFNFIYVEAFKEWEEDP 120
QY 121 NNPATRTRVIDRFRILDGLLERDIPSFRISSGFVEPLLSVYAAANLHAILRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSFRISSGFVEPLLSVYAAANLHAILRDSVIFGER 180
QY 181 WGLTITNVNENYRLIRHIDEYADHCANTYNRGLNLPKSTYQDMITTYNRLRDLTLTVL 240

Db 181 WGLTTINVENYNNRLIRHIDEYANHCADTYNRLGNLNLKSTYQDMWITYNRLRDLTLTVL 240
QY 241 DIAAFPNNYNNRYPIQPVGQLTREVYTDPLNFPNQLQSVLAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFPNNYNNRYPIQPVGQLTREVYTDPLNFPNQLQSVLAQLPTFNWESSAIRNPHL 300
QY 301 FDLNNLTITFTDWFSGVGRNPFYWGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGVPV 360
Db 301 FDLNNLTITFTDWFSGVGRNPFYWGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGVPV 360
QY 361 FRTLSIPTLRLLQOQPCORHFNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPDNSVP 420
Db 361 FRTLSIPTLRLLQOQPCORHFNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPELTTCGVFVSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTTCGVFVSWTHRSATLNTIDPERINQIPLVKAFNLTS 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
Db 481 GTSVVRGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
QY 541 STVGGOVSVNMPLQKMEIGENLTSTRTYRFDSPNPPSFRANPDIIGISEQPLFCAG-S 599
Db 534 STVGSGTGNQGFSTMSANGALTSQSFRFAPP-----VGISAGSQGASIS 582
QY 600 ISSG-----ELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYDHIQ 655
Db 583 ISNVGRQMFHLDRIEFLPVTSTFEEYDLERAQKAVNALFTSTNQIGLKTVDYDHIQ 642
QY 656 VSNLVDCLSEFCLDEKRELSKVHAKRLSDERNLLQDPNFRGINQPDRCWRGSTDIT 715
Db 643 VSNLVECLSEFCLDEKRELSKVHAKRLSDERNLLQDPNFRSINGQLDRCWRGSTDIT 702
QY 716 IQGDDVFKENVYTLPGTVDCEVPTLYOKIDESKLKATRYELRGYIEDSODLEYLIA 775
Db 703 IQGDDVFKENVYTLPGTVDCEVPTLYOKIDESKLKATRYELRGYIEDSODLEYLIYLR 762
QY 776 YNAKHEIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
Db 763 YNAKHEIVNVPGTSLWPLSIENSIGPCGEPNRCAPHLEWNPDLDCSC 810

RESULT 4
JC7140
prototoxin - Bacillus thuringiensis
N:Alternate names: cryIC protein
C:Species: Bacillus thuringiensis
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C:Accession: JC7140
R:Christov, N.K.; Imaishi, H.; Ohkawa, H.
Biosci. Biotechnol. Biochem. 63, 1433-1444, 1999
A:Title: Green-tissue-specific expression of a reconstructed cryIC gene encoding the actin protein.
A:Reference number: JC7140; MUID:99430790; PMID:10501003
A:Accession: JC7140
A:Molecule type: DNA
A:Residues: 1-655 <CHR>
A:Cross-references: EMBL:X96682
C:Genetics:
A:Gene: cryIC
C:Superfamily: parasporal crystal protein

Query Match 77.4%; Score 3374; DB 2; Length 655;
Best Local Similarity 98.9%; Pred. No. 4.2e-236;
Matches 647; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MEENQNCQIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENQNCQIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWIGVPSQWDAFLVQIEQLINERIAAFARNAAIANLEGNNFNFIYVEAFKEWEDP 120

Db 61 DFVWIGVPSQWDAFLVQIEQLINERIAAFARNAAIANLEGNNFNFIYVEAFKEWEDP 120
QY 121 NNPAATRTVIDRFRILDLGLLDRDIPSFRISSGEVPLLSVYAAQANLHLAILRDSVIFGSR 180
Db 121 NNPAATRTVIDRFRILDLGLLDRDIPSFRISSGEVPLLSVYAAQANLHLAILRDSVIFGSR 180
QY 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNRGLNANLPKSTYQDMWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNNRGLNANLPKSTYQDMWITYNRLRDLTLTVL 240
QY 241 DIAAFPNNYNNRYPIQPVGQLTREVYTDPLNFPNQLQSVLAQLPTFNWESSAIRNPHL 300
Db 241 DIAAFPNNYNNRYPIQPVGQLTREVYTDPLNFPNQLQSVLAQLPTFNWESSAIRNPHL 300
QY 301 FDLNNLTITFTDWFSGVGRNPFYWGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGVPV 360
Db 301 FDLNNLTITFTDWFSGVGRNPFYWGCHRVISLIGCGNITSPIYGRANQBPSPFTFNGVPV 360
QY 361 FRTLSIPTLRLLQOQPCORHFNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPDNSVP 420
Db 361 FRTLSIPTLRLLQOQPCORHFNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTPELTTCGVFVSWTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTTCGVFVSWTHRSATLNTIDPERINQIPLVKGRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFYASSRDARVILVTGAA 540
QY 541 STVGGOVSVNMPLQKMEIGENLTSTRTYRFDSPNPPSFRANPDIIGISEQPLFCAGSI 600
Db 541 STVGGOVSVNMPLQKMEIGENLTSTRTYRFDSPNPPSFRANPDIIGISEQPLFCAGSI 600
QY 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYDHI 654
Db 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYDHI 654

RESULT 5
A37829
parasporal crystal protein cryIaI - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 14-Jun-1991 #sequence_revision 03-May-1994 #text_change 01-Dec-2000
C:Accession: A37829; S13762; S14438
R:Visser, B.; Munsterman, E.; Stoker, A.; Dirkse, W.G.
J. Bacteriol. 172, 6783-6788, 1990
A:Title: A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-specific cryIaI
A:Reference number: A37829; MUID:91072224; PMID:2254254
A:Accession: A37829
A:Molecule type: DNA
A:Residues: 1-1171 <VL2>
A:Cross-references: EMBL:X53985
A:Note: translation is incomplete
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 61.5%; Score 2680; DB 2; Length 1171;
Best Local Similarity 64.5%; Pred. No. 2e-185;
Matches 536; Conservative 88; Mismatches 169; Indels 38; Gaps 15;

QY 4 NNQNCQIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLIDF 62
Db 5 NNQNCQIPYNCNLSNPEVLLDIER---SNSVATNIALEISRLASATPIGIGLGLFPA 61
QY 63 VWIGVPSQWDAFLVQIEQLINERIAAFARNAAIANLEGNNFNFIYVEAFKEWEDPNN 122
Db 62 IWGSGPSQWDLFLEQIEILLDQKIEEFARQAISRLGSLGSLYGIYTEAFREWEADPTN 121
QY 123 PATRTVIDRFRILDLGLLDRDIPSFRISSGEVPLLSVYAAQANLHLAILRDSVIFGSR 182
Db 122 PALKEEMRTQPDNMNSILVTAIPLFVSQVQVPLFVSVAQANLHLSVLDRDVSFVGQAWG 181

183 LTTNNVNNYRLIRHIDEVADHCANTYNGRLNLPKS--TYQDWITYNLRDLTLTVLD 241
182 FDIATINSRYNDLTLLPIYDVAWRWNTGLDRLPTGRLNRWAFNQFRELTVSLD 241
242 IAAFFPNYDNRRIPIQVQGLTREVYDPLINFPQSQVAQLPTNVWESSAARNHPLF 301
242 IISFPNYDSRLPIPTSSQLTREVYDPLINFPQSQVAQLPTNVWESSAARNHPLF 297
302 DILNNLTFTDWFSGRNFYWGHRVHSLIGGNN--ITSPYIGREANQPPRSP---TFN 357
298 DFLNNLTFTD--LIRGVHYWAGHRTVSHFTSSQVITTPQYGITANAEPRTIAPSTFP 355
358 G--PVFRTLSIPTLRLQPCQRHFNLAGGEGVEFSTPTNS--FTYRGRTVDSITLPLP 414
356 GLNLFYRTLSNPFRRSENITPTLGINV--VQGVGFIOPNNAEVLRSRGTVDLSNELPI 413
415 E-DNSVPPREGYSHRLCHATEFVQSGTPTLTTGVVFSWTHRSATLNTIDPERINQIPLV 473
414 DGENSL---VGYSHRLSHVTLTRSLYNTNITSLPTFVWTHRSATNTINPDIIITQIPLV 470
474 KGRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARV 533
471 KGRFLGGTSVINGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARI 530
534 IVLTAASGTGSGVSNVMPLOKTMIEIGENLTSTRTFYTFDSNPFSPFRANPDIIIGISEQ- 592
531 TV-----AIGQIRVDMTLEKTMIEIGESLTSRTFSYTNFSPFRANPDIIIRIAEL 583
593 PLFGAGSISGGLYDKIEILADATFEAESDLERAQKAVNALFTSNQIGLKTVDVTDYH 652
584 PIRG-----GELYDKIELILADATFEEDYDLERAQKAVNALFTSNQIGLKTVDVTDYH 637
653 IDQVSNLVDCSDEFCLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGRT 712
638 IDQVSNLVDCSDEFCLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGRT 697
713 DITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDSKLKATYRELGRYEDSDLEIY 772
698 DITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDSKLKATYRELGRYEDSDLEIY 757
773 LIYNAKHETVNVPGTSGSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 823
758 LIRYNAKHETVNVPGTSGSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 808

RESULT 6
140572
paraaporal crystal protein cryICb - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 01-Dec-2000
C:Accession: I40572
R:Boese, M.; Masson, L.; Brouseau, R.
Nucleic Acids Res. 18, 7443, 1990
A:Title: Nucleotide sequence of a novel crystal protein gene isolated from Bacillus thuringiensis
A:Reference number: I40572; MUID:91081338; PMID:2259636
A:Accession: I40572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1171 <RES>
A:Cross-references: EMBL:X56144; NID:G40281; PIDN:CAA39609.1; PID:G40282
C:Gene: cryICb
C:Superfamily: paraaporal crystal protein
C:Keywords: delta-endotoxin

Query Match 61.5%; Score 2680; DB 2; Length 1171;
Best Local Similarity 64.5%; Pred. No. 2e-185;
Matches 536; Conservative 88; Mismatches 169; Indels 38; Gaps 15;

4 NNQNCIPNCLSNPVEVLDERISTGNSIDISLSL-VQELVSNFVPGGELVGLIDP 62
5 NNQNCVPYNNLPENELIDIER---SNSIVATNIAELISRLLSAATPIGILLGLFIDA 61

63 VMGIVGSPQWDAFLVQIEQLINERIAEFARNAANLANLEGLGNFNFIYVAFKWEEDPNN 122
62 IMGSGPQWDAFLVQIEQLINERIAEFARNAANLANLEGLGNFIYVAFKWEEDPNN 121
123 PATRTRVDRFRILDLGLLDERIDPSRISGFEPVLLSVYQAANLHLAILRDSVIFGRWG 182
122 PALKEEMRTQFNDMNSILVTAIPLPSVQNYQVPLSVYQAANLHLAILRDSVIFGRWG 181
183 LTTNNVNNYRLIRHIDEVADHCANTYNGRLNLPKS--TYQDWITYNLRDLTLTVLD 241
182 FDIATINSRYNDLTLLPIYDVAWRWNTGLDRLPTGRLNRWAFNQFRELTVSLD 241
242 IAAFFPNYDNRRIPIQVQGLTREVYDPLINFPQSQVAQLPTNVWESSAARNHPLF 301
242 IISFPNYDSRLPIPTSSQLTREVYDPLINFPQSQVAQLPTNVWESSAARNHPLF 297
302 DILNNLTFTDWFSGRNFYWGHRVHSLIGGNN--ITSPYIGREANQPPRSP---TFN 357
298 DFLNNLTFTD--LIRGVHYWAGHRTVSHFTSSQVITTPQYGITANAEPRTIAPSTFP 355
358 G--PVFRTLSIPTLRLQPCQRHFNLAGGEGVEFSTPTNS--FTYRGRTVDSITLPLP 414
356 GLNLFYRTLSNPFRRSENITPTLGINV--VQGVGFIOPNNAEVLRSRGTVDLSNELPI 413
415 E-DNSVPPREGYSHRLCHATEFVQSGTPTLTTGVVFSWTHRSATLNTIDPERINQIPLV 473
414 DGENSL---VGYSHRLSHVTLTRSLYNTNITSLPTFVWTHRSATNTINPDIIITQIPLV 470
474 KGRVWGGTSVITGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARV 533
471 KGRFLGGTSVINGPGFTGGDILRRNTFGDFVSLQVNSPITQRYRLFRYASSRDARI 530
534 IVLTAASGTGSGVSNVMPLOKTMIEIGENLTSTRTFYTFDSNPFSPFRANPDIIIGISEQ- 592
531 TV-----AIGQIRVDMTLEKTMIEIGESLTSRTFSYTNFSPFRANPDIIIRIAEL 583
593 PLFGAGSISGGLYDKIEILADATFEAESDLERAQKAVNALFTSNQIGLKTVDVTDYH 652
584 PIRG-----GELYDKIELILADATFEEDYDLERAQKAVNALFTSNQIGLKTVDVTDYH 637
653 IDQVSNLVDCSDEFCLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGRT 712
638 IDQVSNLVDCSDEFCLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGRT 697
713 DITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDSKLKATYRELGRYEDSDLEIY 772
698 DITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDSKLKATYRELGRYEDSDLEIY 757
773 LIYNAKHETVNVPGTSGSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 823
758 LIRYNAKHETVNVPGTSGSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 808

RESULT 7
S32647
paraaporal crystal protein cryIb1 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S32647
R:Lambert, B.
submitted to the EMBL Data Library, April 1993
A:Reference number: S32645
A:Accession: S32647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1160 <LAM>
A:Cross-references: EMBL:Z22511; NID:G295863; PIDN:CAA80234.1; PID:G295864
C:Superfamily: paraaporal crystal protein
C:Keywords: delta-endotoxin

Query Match 59.3%; Score 2584; DB 2; Length 1160;
Best Local Similarity 61.9%; Pred. No. 1.8e-178;
Matches 513; Conservative 80; Mismatches 200; Indels 36; Gaps 12;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:22:04 ; Search time 32 Seconds
(without alignments)
1088.182 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNONQICPYNCLNPBE.....GEPNRCAPHLEWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4358	100.0	823	1	Sequence 2, Appli
2	4358	100.0	823	4	Sequence 2, Appli
3	4294	98.5	1189	6	Patent No. 5188960
4	4289	98.4	1189	1	Sequence 2, Appli
5	4289	98.4	1189	2	Sequence 12, Appl
6	4289	98.4	1189	2	Sequence 12, Appl
7	4289	98.4	1189	3	Sequence 12, Appl
8	4289	98.4	1189	3	Sequence 12, Appl
9	4289	98.4	1189	3	Sequence 12, Appl
10	4289	98.4	1189	3	Sequence 12, Appl
11	4289	98.4	1189	4	Sequence 12, Appl
12	4289	98.4	1189	4	Sequence 12, Appl
13	4288	98.4	1189	1	Sequence 16, Appl
14	4288	98.4	1189	1	Sequence 6, Appli
15	4288	98.4	1189	2	Sequence 6, Appli
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25	4288	98.4	1189	3	Sequence 6, Appli
26	4288	98.4	1189	4	Sequence 6, Appli
27	4288	98.4	1189	4	Sequence 6, Appli

28	4288	98.4	1189	4	US-09-337-280-2	Sequence 2, Appli
29	4288	98.4	1189	4	US-09-337-280-6	Sequence 6, Appli
30	4288	98.4	1189	4	US-09-521-344-6	Sequence 6, Appli
31	4288	98.4	1189	5	PCT-US92-11337-16	Sequence 16, Appl
32	4287	98.4	1189	2	US-08-980-071-4	Sequence 4, Appli
33	4287	98.4	1189	2	US-08-757-536-4	Sequence 4, Appli
34	4287	98.4	1189	3	US-09-314-093-4	Sequence 4, Appli
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36	4287	98.4	1189	3	US-09-251-885-4	Sequence 4, Appli
37	4287	98.4	1189	4	US-09-337-635-4	Sequence 4, Appli
38	4287	98.4	1189	4	US-09-337-280-4	Sequence 4, Appli
39	4283	98.3	1189	2	US-08-980-071-10	Sequence 10, Appl
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42	4283	98.3	1189	3	US-09-250-848-10	Sequence 10, Appl
43	4283	98.3	1189	3	US-09-251-885-10	Sequence 10, Appl
44	4283	98.3	1189	4	US-09-337-635-10	Sequence 10, Appl
45	4283	98.3	1189	4	US-09-337-280-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-461-551-2
; Sequence 2, Application US/08461551
; Patent No. 5792928

GENERAL INFORMATION:

APPLICANT: SANCHEZ, Vincent
APPLICANT: LERECLOS, Didier
APPLICANT: MENOU, Ghislaine
APPLICANT: LECADET, Marguerite-Marie
APPLICANT: MARTOURET, Daniel
APPLICANT: DEPONDER, Raymond

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR

TITLE OF INVENTION: LEPIDOPTERA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,551
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,652
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/458,754
FILING DATE: 11-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 88 401 121.4
FILING DATE: 06-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 87 08090
FILING DATE: 10-JUN-1987
ATTORNEY/AGENT INFORMATION:
NAME: HUNTINGTON, R. D.
REGISTRATION NUMBER: 27,903
REFERENCE/DOCKET NUMBER: 010830-073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021


```
QY 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLOQVAQLPTFNWMESSAIRNPHL 300
Db 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLOQVAQLPTFNWMESSAIRNPHL 300
QY 301 FOILNNLTFTDWFSGVGRNFGYGHVRVSSLLGGNITSPYIGREANQEPFRFTNGPV 360
Db 301 FOILNNLTFTDWFSGVGRNFGYGHVRVSSLLGGNITSPYIGREANQEPFRFTNGPV 360
QY 361 FRTLSTPTLRLLOQPQCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
Db 361 FRTLSTPTLRLLOQPQCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTFFLTGTVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
Db 421 PREGYSHRLCHATFVQSGTFFLTGTVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
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QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
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QY 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 3
5188960-6
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,261
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 371,955
; FILING DATE: 27-JUN-1989
; SEQ ID NO: 6:
; LENGTH: 1189
5188960-6

Query Match 98.5%; Score 4294; DB 6; Length 1189;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 815; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1 MEENNQICYPNCLSNPEVLLDGERISTGNSSIDISLQVFLVSNFVPGGFLVGLI 60
QY 61 DFWGIVGSPQDFAFLVQIEQLINERIAAFARNAAIANLEGGLNNFNIIYVEAFKWEEDP 120
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Db 61 DFWGIVGSPQDFAFLVQIEQLINERIAAFARNAAIANLEGGLNNFNIIYVEAFKWEEDP 120
QY 121 NNPATRVIDFRILDGLLEDRIDPSFRISGPEVPLLSVVAQANLHLAILRDSVIFGER 180
Db 121 NNPATRVIDFRILDGLLEDRIDPSFRISGPEVPLLSVVAQANLHLAILRDSVIFGER 180
QY 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENNRLIRHIDEYADHCANTYNGRLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLOQVAQLPTFNWMESSAIRNPHL 300
Db 241 DIAAFFPNYDNRYPQPVQQLTREYVTDPLINFNPOLOQVAQLPTFNWMESSAIRNPHL 300
QY 301 FOILNNLTFTDWFSGVGRNFGYGHVRVSSLLGGNITSPYIGREANQEPFRFTNGPV 360
Db 301 FOILNNLTFTDWFSGVGRNFGYGHVRVSSLLGGNITSPYIGREANQEPFRFTNGPV 360
QY 361 FRTLSTPTLRLLOQPQCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
Db 361 FRTLSTPTLRLLOQPQCORHHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTFFLTGTVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
Db 421 PREGYSHRLCHATFVQSGTFFLTGTVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
QY 541 STGVGGQVSNMPLQKTMGEIGENLTSTRFTYDFFSNPFSFRANPDIIGISEQPLFCAGSI 600
Db 541 STGVGGQVSNMPLQKTMGEIGENLTSTRFTYDFFSNPFSFRANPDIIGISEQPLFCAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLKTVDYDHYDQVSNLV 660
QY 661 DCLSDFCDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIQGGD 720
Db 661 DCLSDFCDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDTITIQGGD 720
QY 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLAIYNAKH 780
Db 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLAIYNAKH 780
QY 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 4
US-08-602-737-2
; Sequence 2, Application US/08602737
; Patent No. 5736131
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J
; APPLICANT: Stiekema, Willem J
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SANDOZ AGRO, INC
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: CA 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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us-09-918-485-2.ra1

Wed Oct 15 11:56:18 2003

APPLICATION NUMBER: US/08/602,737
FILING DATE: 21-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 130-4080
TELEPHONE: 415-354-3588
TELEFAX: 415-857-1125
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-602-737-2

Query Match 98.4%; Score 4289; DB 1; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 MEENNQOCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
DB 1 MEENNQOCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
QY 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAKWEEDP 120
DB 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAKWEEDP 120
QY 121 NNPAATRVDRFRILDGLLDRDIPSPRISGFVEPVLSSVYQAANLHAILRDSVIFGER 180
DB 121 NNPAATRVDRFRILDGLLDRDIPSPRISGFVEPVLSSVYQAANLHAILRDSVIFGER 180
QY 181 WGLTTINVENYNNELIRHIDEVADHCANTYNRGLNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTINVENYNNELIRHIDEVADHCANTYNRGLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFPYNDNRRYPIQVQOLTREVYTDPLINFPOLQSAQLPTFNWESSAIRNPHL 300
DB 241 DIAAFPYNDNRRYPIQVQOLTREVYTDPLINFPOLQSAQLPTFNWESSAIRNPHL 300
QY 301 FDLNNLITFTDFSVGRNFGYGHVRVSSLIIGGNTSPYIGREANQEPFRSFTFNGVP 360
DB 301 FDLNNLITFTDFSVGRNFGYGHVRVSSLIIGGNTSPYIGREANQEPFRSFTFNGVP 360
QY 361 FRLTSLPTLRLLQCPQORHHNLRGEGVEFTPTNSFTYRGRGTVDLSITLPPEDNSVP 420
DB 361 FRLTSLPTLRLLQCPQORHHNLRGEGVEFTPTNSFTYRGRGTVDLSITLPPEDNSVP 420
QY 421 PRGYSHRLCHATFVQSGTPELTTCGVFSTHRSATLTNTIDPERINQIPLVKGFRVWG 480
DB 421 PRGYSHRLCHATFVQSGTPELTTCGVFSTHRSATLTNTIDPERINQIPLVKGFRVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNTSPITQRYLRFYVASSRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNTSPITQRYLRFYVASSRDARVILTGAA 540
QY 541 STGVGGQVSNMPLQKTWEIGENLTSTRYTDPSNFRANPDITIGTSGPLFGAGSI 600
DB 541 STGVGGQVSNMPLQKTWEIGENLTSTRYTDPSNFRANPDITIGTSGPLFGAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKDTHDHIQVNSLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKDTHDHIQVNSLV 660
QY 661 DCLDEFCLDKRELSEKVKIAKLSDERNLLQDPNFRGNRPQDRGWSGTDITIOGGD 720
DB 661 DCLDEFCLDKRELSEKVKIAKLSDERNLLQDPNFRGNRPQDRGWSGTDITIOGGD 720
QY 721 DVFENKVVTLPGTVDECYPTLYQKIDESKIKAYTRYELRGYIEDSQDLEIYLIAYNKX 780
DB 721 DVFENKVVTLPGTVDECYPTLYQKIDESKIKAYTRYELRGYIEDSQDLEIYLIAYNKX 780

QY 781 EIVNVPGTSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSC 823

RESULT 5
US-08-980-071-12 Application US/08980071
Sequence 12 Patent No. 5914318
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Glimer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-071-12

Query Match 98.4%; Score 4289; DB 2; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQOCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
DB 1 MEENNQOCIPYCLNPEEVLDDGERISTGNSIDISLSVQLVSNFVPGGGLVGLI 60
QY 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAKWEEDP 120
DB 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAATANLEGLGNFNLYVEAKWEEDP 120
QY 121 NNPAATRVDRFRILDGLLDRDIPSPRISGFVEPVLSSVYQAANLHAILRDSVIFGER 180
DB 121 NNPAATRVDRFRILDGLLDRDIPSPRISGFVEPVLSSVYQAANLHAILRDSVIFGER 180
QY 181 WGLTTINVENYNNELIRHIDEVADHCANTYNRGLNLPKSTYQDMITYNRLRDLTLTVL 240
DB 181 WGLTTINVENYNNELIRHIDEVADHCANTYNRGLNLPKSTYQDMITYNRLRDLTLTVL 240
QY 241 DIAAFPYNDNRRYPIQVQOLTREVYTDPLINFPOLQSAQLPTFNWESSAIRNPHL 300
DB 241 DIAAFPYNDNRRYPIQVQOLTREVYTDPLINFPOLQSAQLPTFNWESSAIRNPHL 300

Db 241 DIAFFPNYDNRYPQVQQLTRVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGGNITSPYIGREANQEPFRSFTFNGPV 360
Db 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGGNITSPYIGREANQEPFRSFTFNGPV 360
Qy 361 FRTLSIPTLLLOQPQCORHHFNLRGGEGVEFSTPTNSFTYRGRGTWDSLTTELPPEDNSVP 420
Db 361 FRTLSNPTLLLOQPQWAPPFNLRGGEGVEFSTPTNSFTYRGRGTWDSLTTELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG 480
Db 421 PREGYSHRLCHATFVQSRGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG 480
Qy 481 GTSVITGPGTGGDILARNITGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Db 481 GTSVITGPGTGGDILARNITGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Qy 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPFRANPDIIIGSEQPLFGAGSI 600
Db 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPFRANPDIIIGSEQPLFGAGSI 600
Qy 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINQPDRCGRGSTDTITIQGGD 720
Db 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINQPDRCGRGSTDTITIQGGD 720
Qy 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLIRYNAKH 780
Db 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 6
US-08-757-536-12
; Sequence 12, Application US/08757536
; Patent No. 5942664
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Gilmer, Amy Jelen
; APPLICANT: Mettus, Anne-Marie Light
; TITLE OF INVENTION: Bacillus thuringiensis Cryic
; TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
; TITLE OF INVENTION: Making Cryic Mutants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White and Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,536
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-757-536-12

Query Match 98.4%; Score 4289; DB 2; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MEENNQNCIPYCNLSNPEEVLIDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNQNCIPYCNLSNPEEVLIDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGNNFNIIYVEAFKWEEDP 120
Db 61 DFWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGNNFNIIYVEAFKWEEDP 120
Qy 121 NNPAFTRVIDRFRILDLGLERDIPSFRIISGEFVPLLSVYAAANLHLAIRDVSIFGR 180
Db 121 NNPAFTRVIDRFRILDLGLERDIPSFRIISGEFVPLLSVYAAANLHLAIRDVSIFGR 180
Qy 181 WGLTTINNVNENYRLIRIHIDEVADHCANTYRGLNANLPKSTYQDMITYNRLRDLTLTVL 240
Db 181 WGLTTINNVNENYRLIRIHIDEVADHCANTYRGLNANLPKSTYQDMITYNRLRDLTLTVL 240
Qy 241 DIAAFPNYDNRYPQVQQLTRVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFPNYDNRYPQVQQLTRVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGGNITSPYIGREANQEPFRSFTFNGPV 360
Db 301 FDILNNLTITDWFSGVGRNFWGHRVVISSILGGNITSPYIGREANQEPFRSFTFNGPV 360
Qy 361 FRTLSIPTLLLOQPQCORHHFNLRGGEGVEFSTPTNSFTYRGRGTWDSLTTELPPEDNSVP 420
Db 361 FRTLSNPTLLLOQPQWAPPFNLRGGEGVEFSTPTNSFTYRGRGTWDSLTTELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSRGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG 480
Db 421 PREGYSHRLCHATFVQSRGTPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG 480
Qy 481 GTSVITGPGTGGDILARNITGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
Db 481 GTSVITGPGTGGDILARNITGDFVSLQVNNINSPIQRYELRFRYASSRDARVIVLTGAA 540
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Db 541 STGVGGQSVNMPLOKTMELGENLTSTRTFRYTDPSNPFSPFRANPDIIIGSEQPLFGAGSI 600
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Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINQPDRCGRGSTDTITIQGGD 720
Db 661 DCLSDFCLEKRELSKVKHAKRLSDERNLLQDPNFRGINQPDRCGRGSTDTITIQGGD 720
Qy 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLIRYNAKH 780
Db 721 DVFKNYVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 7
US-09-314-093-12
; Sequence 12, Application US/09314093

Wed Oct 15 11:56:18 2003

Patent No. 6033874
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/980,071
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-314-093-12

Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY	1	MEENNQCIPYNCLSNP	EVLLDGERISTGNS	SIDISLSVQFLVSNFVPGGFLVGLI	60		
DB	1	MEENNQCIPYNCLSNP <td>EVLLDGERISTGNS<td>SIDISLSVQFLVSNFVPGGFLVGLI<td>60</td></td></td>	EVLLDGERISTGNS <td>SIDISLSVQFLVSNFVPGGFLVGLI<td>60</td></td>	SIDISLSVQFLVSNFVPGGFLVGLI <td>60</td>	60		
QY	61	DFVWGIVGPSQWDAFL	QVIOBOLINERIAE	FAFARNAAIANLEGL	NNFNFIYVEAFKEWEDP	120	
DB	61	DFVWGIVGPSQWDAFL	QVIOBOLINERIAE	FAFARNAAIANLEGL	NNFNFIYVEAFKEWEDP	120	
QY	121	NPDATETVIDRFRIL	QGLERDIPSRISG	FEVPLLSVYQAANL	HLAIRDVSIFIGER	180	
DB	121	NPDATETVIDRFRIL	QGLERDIPSRISG	FEVPLLSVYQAANL	HLAIRDVSIFIGER	180	
QY	181	WGLTTINNVNENRIL	ISHIDEVADHCANTY	RGNLNPSTYQDMIT	TYNRLRDLTLTVL	240	
DB	181	WGLTTINNVNENRIL	ISHIDEVADHCANTY	RGNLNPSTYQDMIT	TYNRLRDLTLTVL	240	
QY	241	DIAAFPYNDNRPIQ	VPQQLTREVYTDPL	INFNPOLQSVACL	PTFNWMESSAIRNPHL	300	
DB	241	DIAAFPYNDNRPIQ	VPQQLTREVYTDPL	INFNPOLQSVACL	PTFNWMESSAIRNPHL	300	
QY	301	FDILNNLTITFTD	WFSVGNFVWGGHVI	SSLIQGNITSYIG	REANQBPFRSTFNGPV	360	
DB	301	FDILNNLTITFTD	WFSVGNFVWGGHVI	SSLIQGNITSYIG	REANQBPFRSTFNGPV	360	
QY	361	FRTLISPTLRLLQ	QPCORHHFNLRG	SGEVFTPTFNGST	YRGTGVDLSITELP	EDNSVP	420
DB	361	FRTLISPTLRLLQ	QPCORHHFNLRG	SGEVFTPTFNGST	YRGTGVDLSITELP	EDNSVP	420

QY	421	PREGYSHRLCHATE	FVQSRGTPFLT	TCVVVFSWTHRSAT	LTNTIDPRINQIPLVKGPRVWG	480
DB	421 <th>PREGYSHRLCHATE</th> <th>FVQSRGTPFLT</th> <th>TCVVVFSWTHRSAT</th> <th>LTNTIDPRINQIPLVKGPRVWG</th> <th>480</th>	PREGYSHRLCHATE	FVQSRGTPFLT	TCVVVFSWTHRSAT	LTNTIDPRINQIPLVKGPRVWG	480
QY	481 <th>GTSVITGPGFTGGD</th> <th>ILARNNTFGDFV</th> <th>SLQVNIINSPI</th> <th>TQYRLARFRYASSRDRARVIVLTGAA</th> <th>540</th>	GTSVITGPGFTGGD	ILARNNTFGDFV	SLQVNIINSPI	TQYRLARFRYASSRDRARVIVLTGAA	540
DB	481 <th>GTSVITGPGFTGGD</th> <th>ILARNNTFGDFV</th> <th>SLQVNIINSPI</th> <th>TQYRLARFRYASSRDRARVIVLTGAA</th> <th>540</th>	GTSVITGPGFTGGD	ILARNNTFGDFV	SLQVNIINSPI	TQYRLARFRYASSRDRARVIVLTGAA	540
QY	541 <th>STGVGGQVSNVPL</th> <th>QKTMWIGENL</th> <th>TSRTFRVTFDSN</th> <th>PFSPRANPDIIIGISQPLFGAGSI</th> <th>600</th>	STGVGGQVSNVPL	QKTMWIGENL	TSRTFRVTFDSN	PFSPRANPDIIIGISQPLFGAGSI	600
DB	541 <th>STGVGGQVSNVPL</th> <th>QKTMWIGENL</th> <th>TSRTFRVTFDSN</th> <th>PFSPRANPDIIIGISQPLFGAGSI</th> <th>600</th>	STGVGGQVSNVPL	QKTMWIGENL	TSRTFRVTFDSN	PFSPRANPDIIIGISQPLFGAGSI	600
QY	601 <th>SSGELYIDKIELI</th> <th>ILLADATPEAESD</th> <th>LERAQKAVNAL</th> <th>FTSSNQIGLTKTDVTDYHIDQVSNLV</th> <th>660</th>	SSGELYIDKIELI	ILLADATPEAESD	LERAQKAVNAL	FTSSNQIGLTKTDVTDYHIDQVSNLV	660
DB	601 <th>SSGELYIDKIELI</th> <th>ILLADATPEAESD</th> <th>LERAQKAVNAL</th> <th>FTSSNQIGLTKTDVTDYHIDQVSNLV</th> <th>660</th>	SSGELYIDKIELI	ILLADATPEAESD	LERAQKAVNAL	FTSSNQIGLTKTDVTDYHIDQVSNLV	660
QY	661 <th>DCLSDPFLDREK</th> <th>SELSEKVKHAK</th> <th>SDRENLLQDPN</th> <th>FRGINROPDRGWRGSTDITIOGGD</th> <th>720</th>	DCLSDPFLDREK	SELSEKVKHAK	SDRENLLQDPN	FRGINROPDRGWRGSTDITIOGGD	720
DB	661 <th>DCLSDPFLDREK</th> <th>SELSEKVKHAK</th> <th>SDRENLLQDPN</th> <th>FRGINROPDRGWRGSTDITIOGGD</th> <th>720</th>	DCLSDPFLDREK	SELSEKVKHAK	SDRENLLQDPN	FRGINROPDRGWRGSTDITIOGGD	720
QY	721 <th>DVFKENYVTLPG</th> <th>TVDDECYPYLY</th> <th>QKIDESKLYAT</th> <th>RYELRGYIETDSODLEIYLLIAYNAKH</th> <th>780</th>	DVFKENYVTLPG	TVDDECYPYLY	QKIDESKLYAT	RYELRGYIETDSODLEIYLLIAYNAKH	780
DB	721 <th>DVFKENYVTLPG</th> <th>TVDDECYPYLY</th> <th>QKIDESKLYAT</th> <th>RYELRGYIETDSODLEIYLLIAYNAKH</th> <th>780</th>	DVFKENYVTLPG	TVDDECYPYLY	QKIDESKLYAT	RYELRGYIETDSODLEIYLLIAYNAKH	780
QY	781 <th>EIVNVFCTGSL</th> <th>WPLSAQSP</th> <th>IGKCGEPNRCAP</th> <th>HLWNPDLDSC</th> <th>823</th>	EIVNVFCTGSL	WPLSAQSP	IGKCGEPNRCAP	HLWNPDLDSC	823
DB	781 <th>EIVNVFCTGSL</th> <th>WPLSAQSP</th> <th>IGKCGEPNRCAP</th> <th>HLWNPDLDSC</th> <th>823</th>	EIVNVFCTGSL	WPLSAQSP	IGKCGEPNRCAP	HLWNPDLDSC	823

RESULT 8
US-09-250-848-12
Sequence 12, Application US/09250848
Patent No. 6153814
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: Bacillus thuringiensis Cry1C
TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
TITLE OF INVENTION: Making Cry1C Mutants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX USA
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/250,848
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,536
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOST:023
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-250-848-12

Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPYNCISNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYNCISNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
DB 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYAQAANLHLAIRDSDVIFGER 180
DB 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYAQAANLHLAIRDSDVIFGER 180
QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFPNYDNRYPPIQPVQOLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
DB 241 DIAAFPNYDNRYPPIQPVQOLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
QY 301 FDIILNLTITDWFSGVGRNFGVGHVVISLIGGNTSPYIGREANQEPFRFTFNGPV 360
DB 301 FDIILNLTITDWFSGVGRNFGVGHVVISLIGGNTSPYIGREANQEPFRFTFNGPV 360
QY 361 FRTLSIPTLRLLQOQPCORHHFNLRGGEVGFSTPTNSFTYRGRTVDSLTPELPPEDNSVP 420
DB 361 FRTLSIPTLRLLQOQPCORHHFNLRGGEVGFSTPTNSFTYRGRTVDSLTPELPPEDNSVP 420
QY 421 PREGYSHRLCHATFVQRSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFVRWG 480
DB 421 PREGYSHRLCHATFVQRSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFVRWG 480
QY 481 GTSVITGPGTGGDILRRNTFGFVSLQVNNINSPIQRYRLRFRYASRRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGFVSLQVNNINSPIQRYRLRFRYASRRDARVILTGAA 540
QY 541 STGVGGQVSNMPLQKTMIEIGENLTSTPRYTDFSNPFSFRANPDIIIGISEQLFGAGSI 600
DB 541 STGVGGQVSNMPLQKTMIEIGENLTSTPRYTDFSNPFSFRANPDIIIGISEQLFGAGSI 600
QY 601 SSGELYIDKIEIILADATPAESDLERAQKAVNALFTSSNQIGLKTVDYTHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATPAESDLERAQKAVNALFTSSNQIGLKTVDYTHIDQVSNLV 660
QY 661 DCLSDPCLDEKELSEKVKHAKRLSDERNLLQDPNFRGNINRQPDGRGSGTDITIQGGD 720
DB 661 DCLSDPCLDEKELSEKVKHAKRLSDERNLLQDPNFRGNINRQPDGRGSGTDITIQGGD 720
QY 721 DVPKENYVTLPGTVDECPYLYQKIDESKLAATRYELAGYIEDSQDLEIYLIYNAXH 780
DB 721 DVPKENYVTLPGTVDECPYLYQKIDESKLAATRYELAGYIEDSQDLEIYLIYNAXH 780
QY 781 EIVNVFGTSLWPLSAQSPKGCGBNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVFGTSLWPLSAQSPKGCGBNRCAPHLEWNPDLDCSC 823

RESULT 9

US-09-251-885-12
Sequence 12, Application US/09251885
Patent No. 6177615
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Amy Jelen
APPLICANT: Mettus, Anne-Marie Light
TITLE OF INVENTION: Bacillus thuringiensis CryIc

TITLE OF INVENTION: Compositions Toxic to Lepidopteran Insects and Methods for
TITLE OF INVENTION: Making CryIc Mutants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White and Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,885
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,536
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBT:023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-251-885-12

Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPYNCISNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYNCISNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
DB 61 DFVWGVGPSQWDAFLVQIOLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYAQAANLHLAIRDSDVIFGER 180
DB 121 NNPATRTRVIDRFRILDLGLERDIPSRISGFEVPLLSVYAQAANLHLAIRDSDVIFGER 180
QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFPNYDNRYPPIQPVQOLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
DB 241 DIAAFPNYDNRYPPIQPVQOLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
QY 301 FDIILNLTITDWFSGVGRNFGVGHVVISLIGGNTSPYIGREANQEPFRFTFNGPV 360
DB 301 FDIILNLTITDWFSGVGRNFGVGHVVISLIGGNTSPYIGREANQEPFRFTFNGPV 360
QY 361 FRTLSIPTLRLLQOQPCORHHFNLRGGEVGFSTPTNSFTYRGRTVDSLTPELPPEDNSVP 420
DB 361 FRTLSIPTLRLLQOQPCORHHFNLRGGEVGFSTPTNSFTYRGRTVDSLTPELPPEDNSVP 420
QY 421 PREGYSHRLCHATFVQRSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFVRWG 480
DB 421 PREGYSHRLCHATFVQRSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFVRWG 480

QY 481 GTSVITGPGTGGDILRNTFEDFVSLQVNSPITQRYRLRYASSDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRNTFEDFVSLQVNSPITQRYRLRYASSDARVILTGAA 540
QY 541 STVGQGVSNMPLQKMEIGENITSTRTYTDPSNPPSPFRANPDIIIGISEOPLGAGSI 600
DB 541 STVGQGVSNMPLQKMEIGENITSTRTYTDPSNPPSPFRANPDIIIGISEOPLGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTDYHIDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTDYHIDQVSNLV 660
QY 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTIIOGGD 720
DB 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTIIOGGD 720
QY 721 DVFENYVTLPGTVDECYPTVLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
DB 721 DVFENYVTLPGTVDECYPTVLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
QY 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 10

US-09-001-982-2
; Sequence 2, Application US/09001982
; Patent No. 6204246
; GENERAL INFORMATION:
; APPLICANT: Bosch, Hendrick J.
; APPLICANT: Sciekema, Willem J.
; TITLE OF INVENTION: Hybrid Toxin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6204246artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8687
; TELEFAX: 919-541-8687
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-982-2
Query Match 98.4%; Score 4289; DB 3; Length 1189;
Best Local Similarity 98.9%; Pred. NO. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNOQICPNCLSNPEEVLIDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60

DB 1 MEENNOQICPNCLSNPEEVLIDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIIVGSPQWDAFLVQIEQLINERIAEFARNAANLANEGLGNFNFTYVFAFKWEEDP 120
DB 61 DFVWGIIVGSPQWDAFLVQIEQLINERIAEFARNAANLANEGLGNFNFTYVFAFKWEEDP 120
QY 121 NNPAETRTVIDRFRILGDLERDIPFRISGFEVPLLSVYAQAANLHAILLARDSVIFGER 180
DB 121 NNPAETRTVIDRFRILGDLERDIPFRISGFEVPLLSVYAQAANLHAILLARDSVIFGER 180
QY 181 WGLTTNNVNNYNNLIRHIDEVADHCANTYNNRGLNNLPKSTYQDMITTYNNRLRDLITLVL 240
DB 181 WGLTTNNVNNYNNLIRHIDEVADHCANTYNNRGLNNLPKSTYQDMITTYNNRLRDLITLVL 240
QY 241 DIAAFPNYDNRPIQPVQQLREVYTDPLINFNPOLQSVQALPTFNWMESSAIRNPHL 300
DB 241 DIAAFPNYDNRPIQPVQQLREVYTDPLINFNPOLQSVQALPTFNWMESSAIRNPHL 300
QY 301 FDIILNLTITFTDWFSGVGNFWGHRVTSISLIGGNITSPITYGREANQPPRSTFTNGPV 360
DB 301 FDIILNLTITFTDWFSGVGNFWGHRVTSISLIGGNITSPITYGREANQPPRSTFTNGPV 360
QY 361 FRTLSTPTLRLLQPCQRRHHPNLRGGEVFEFTPTNSFTYRGRTVDSLTLPEDNSVP 420
DB 361 FRTLSTPTLRLLQPCQRRHHPNLRGGEVFEFTPTNSFTYRGRTVDSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQRSQTPFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
DB 421 PREGYSHRLCHATFVQRSQTPFTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
QY 481 GTSVITGPGTGGDILRNTFEDFVSLQVNSPITQRYRLRYASSDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRNTFEDFVSLQVNSPITQRYRLRYASSDARVILTGAA 540
QY 541 STVGQGVSNMPLQKMEIGENITSTRTYTDPSNPPSPFRANPDIIIGISEOPLGAGSI 600
DB 541 STVGQGVSNMPLQKMEIGENITSTRTYTDPSNPPSPFRANPDIIIGISEOPLGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTDYHIDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNOIGLTKTDVTDYHIDQVSNLV 660
QY 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTIIOGGD 720
DB 661 DCLSDFCLEKELSEKVKHAKLSDERNLLQDPNFRGINRQPDGRWGSDTIIOGGD 720
QY 721 DVFENYVTLPGTVDECYPTVLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
DB 721 DVFENYVTLPGTVDECYPTVLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIRYNAKH 780
QY 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTGSIMPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 11

US-09-337-635-12
; Sequence 12, Application US/09337635
; Patent No. 6313378
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; Gilmer, Amy Jelen
; Mettus, Anne-Marie Light
; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
; LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA

Db 61 DFVWGVGSQWDAFLVQEQINERIAEFARNAANLEGLGNFNIVYEAFFKEWEDP 120
Qy 121 NNPAITRVIDRILDGLLERDIPSRISGEFVPLLSVYAQAANHLALRDSVIFGER 180
Db 121 NNPAITRVIDRILDGLLERDIPSRISGEFVPLLSVYAQAANHLALRDSVIFGER 180
Qy 181 WGLTTINVENYNRLIRHIDYADHCANTYNGLANLKPSTYQDWITYNRLRDLTLVL 240
Db 181 WGLTTINVENYNRLIRHIDYADHCANTYNGLANLKPSTYQDWITYNRLRDLTLVL 240
Qy 241 DIAAFFPNYDNRYPITQPVQLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYDNRYPITQPVQLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDIILNNLTFTDWFSGVGRNFWGGRHVISLIGGNITSPYIGREANQEPFRSTFNGPV 360
Db 301 FDIILNNLTFTDWFSGVGRNFWGGRHVISLIGGNITSPYIGREANQEPFRSTFNGPV 360
Qy 361 FRTLSIPTLRLLQPCORHFNHNLGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Db 361 FRTLSIPTLRLLQPCORHFNHNLGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSGTPELTITGVVFWSTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTITGVVFWSTHRSATLNTIDPERINQIPLVKGRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYELRFRYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYELRFRYASSRDARVILTGAA 540
Qy 541 STGVGGQSVNMPLOKTMIEGENLTSTRFTYDPSNPFSSFRANPDIIIGSEQPLFAGSI 600
Db 541 STGVGGQSVNMPLOKTMIEGENLTSTRFTYDPSNPFSSFRANPDIIIGSEQPLFAGSI 600
Qy 601 SSGELYIDKIEIILADATPEASDLERAQAVNALTSNQIGLTKTDVTHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATPEASDLERAQAVNALTSNQIGLTKTDVTHIDQVSNLV 660
Qy 661 DCLSEDFCLDEKRELSEKVKHAKRLSDERNLLODPNFRGINQPDGRWGRTDITIQGGD 720
Db 661 DCLSEDFCLDEKRELSEKVKHAKRLSDERNLLODPNFRGINQPDGRWGRTDITIQGGD 720
Qy 721 DVFKENYVTLPGTDECYPTLYQKIDESKIKAYTRYELRGVIEDSQDLBIYLIYNAXH 780
Db 721 DVFKENYVTLPGTDECYPTLYQKIDESKIKAYTRYELRGVIEDSQDLBIYLIYNAXH 780
Qy 781 EIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 13
US-07-828-788A-16
Sequence 16, Application US/07828788A
Patent No. 5273746
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS911
IMMEDIATE SOURCE:
LIBRARY: LAMEDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811B2
US-07-828-788A-16

Query Match 98.4%; Score 4288; DB 1; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MEENNONOCIPYNCNLSNPEEVLDERISTGNSSIDISLSLVQPLVSNFVPGGFLVGLI 60
Db 1 MEENNONOCIPYNCNLSNPEEVLDERISTGNSSIDISLSLVQPLVSNFVPGGFLVGLI 60
Qy 61 DFVWGVGSQWDAFLVQEQINERIAEFARNAANLEGLGNFNIVYEAFFKEWEDP 120
Db 61 DFVWGVGSQWDAFLVQEQINERIAEFARNAANLEGLGNFNIVYEAFFKEWEDP 120
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Db 121 NNPAITRVIDRILDGLLERDIPSRISGEFVPLLSVYAQAANHLALRDSVIFGER 180
Qy 181 WGLTTINVENYNRLIRHIDYADHCANTYNGLANLKPSTYQDWITYNRLRDLTLVL 240
Db 181 WGLTTINVENYNRLIRHIDYADHCANTYNGLANLKPSTYQDWITYNRLRDLTLVL 240
Qy 241 DIAAFFPNYDNRYPITQPVQLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYDNRYPITQPVQLTREVYTDPLINFPOLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDIILNNLTFTDWFSGVGRNFWGGRHVISLIGGNITSPYIGREANQEPFRSTFNGPV 360
Db 301 FDIILNNLTFTDWFSGVGRNFWGGRHVISLIGGNITSPYIGREANQEPFRSTFNGPV 360
Qy 361 FRTLSIPTLRLLQPCORHFNHNLGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Db 361 FRTLSIPTLRLLQPCORHFNHNLGEGVEFSTPTNSFTYGRGTVDLSLTELPPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSGTPELTITGVVFWSTHRSATLNTIDPERINQIPLVKGRVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTITGVVFWSTHRSATLNTIDPERINQIPLVKGRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYELRFRYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNIINSPIQRYELRFRYASSRDARVILTGAA 540
Qy 541 STGVGGQSVNMPLOKTMIEGENLTSTRFTYDPSNPFSSFRANPDIIIGSEQPLFAGSI 600
Db 541 STGVGGQSVNMPLOKTMIEGENLTSTRFTYDPSNPFSSFRANPDIIIGSEQPLFAGSI 600

QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDTVDYHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDTVDYHIDQVSNLV 660
QY 661 DCLSDPECLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGSGTDTITQGGD 720
DB 661 DCLSDPECLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGSGTDTITQGGD 720
QY 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIYANAKH 780
DB 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIYANAKH 780
QY 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 14

US-08-356-034-6
; Sequence 6, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; REGISTRATION NUMBER: 21,023
; REFERENCE/DOCKET NUMBER: MA43.C1.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811B2
; US-08-356-034-6
Query Match 98.4%; Score 4288; DB 1; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNQOCIPYNCLSNPEVLLDGERISTGSSSIDISLSLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQOCIPYNCLSNPEVLLDGERISTGSSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGVGPSQWDALFLVQIEQLINERIASFARNAAIANLEGLNNTNIIYVEAFKEWEDP 120
DB 61 DFVWGVGPSQWDALFLVQIEQLINERIASFARNAAIANLEGLNNTNIIYVEAFKEWEDP 120
QY 121 NNPATRTRVIDRPRILDGLERDIPSFRISSGFEVPLLSVYQAANLHLAILRDSVIFGR 180
DB 121 NNPATRTRVIDRPRILDGLERDIPSFRISSGFEVPLLSVYQAANLHLAILRDSVIFGR 180
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DB 181 WGLTTINNVNENYRLIRHIDEVADHCANTYRGLNLPKSTYQDMITYNRLRDLTLTVL 240
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DB 241 DIAAPPNDNRRYPIQPVQQLTREYTDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
QY 301 FDLANNLTFTDWFSGVRNFGGHRVSSLLGGGNTSPYVCREANQPPRSTFNGPV 360
DB 301 FDLANNLTFTDWFSGVRNFGGHRVSSLLGGGNTSPYVCREANQPPRSTFNGPV 360
QY 361 FRTLSTPLRLQOQCORHFNLRGEGVEFSTPTNSFTYRGRTGTVDSITELPPENSVP 420
DB 361 FRTLSTPLRLQOQCORHFNLRGEGVEFSTPTNSFTYRGRTGTVDSITELPPENSVP 420
QY 421 PREGYSHRLCHATFVQSGTPELTGGVFWFSWTHRSATLNTIDPERINQIPLVKGFVWG 480
DB 421 PREGYSHRLCHATFVQSGTPELTGGVFWFSWTHRSATLNTIDPERINQIPLVKGFVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFRYASSRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSPITQRYLRFRYASSRDARVILTGAA 540
QY 541 STGVGGQSVNMPLOKTEIGENLTSRTPRYTDFSNPFRFRANPDIIGISEOPLFCAGSI 600
DB 541 STGVGGQSVNMPLOKTEIGENLTSRTPRYTDFSNPFRFRANPDIIGISEOPLFCAGSI 600
QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDTVDYHIDQVSNLV 660
DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDTVDYHIDQVSNLV 660
QY 661 DCLSDPECLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGSGTDTITQGGD 720
DB 661 DCLSDPECLDEKRELSKVHAKLSDERNLQDPNFRGINRQPDGRGSGTDTITQGGD 720
QY 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIYANAKH 780
DB 721 DVFKNYVTLPGTVDECPYLYQKIDESKLKAYTRYELRGYIEDSDQLEIYLIYANAKH 780
QY 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 15
US-08-980-071-2

Sequence 2, Application US/08980071
Patent No. 5914318
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Gilmer, Anne Marie Light
APPLICANT: Metcub, Anne-Marie Light
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: LEPIDOPTERAN-ACTIVE-DELTA-ENDOTOXINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,071
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/757,536
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MECO:206
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-071-2

Query Match 98.4%; Score 4288; DB 2; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNQCIPYNCNPNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQCIPYNCNPNPEVLLDGERISTGNSIDISLSVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNPNFIYVEAFKEWEEDP 120
DB 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNPNFIYVEAFKEWEEDP 120
QY 121 NNPA TRTRVIDRPRILDGLLDRIDSPRISGFVEVPLLSVYQAANLHLAIRDSDVIFGER 180
DB 121 NNPA TRTRVIDRPRILDGLLDRIDSPRISGFVEVPLLSVYQAANLHLAIRDSDVIFGER 180
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QY 241 DTAARFNNDRYPYQVQQLTRVYTDPLINPOLQSVACLPTFNWESSAIRNPHL 300
DB 241 DTAARFNNDRYPYQVQQLTRVYTDPLINPOLQSVACLPTFNWESSAIRNPHL 300
QY 301 FDILNNLIFIDWFSVGRNFGYGHVLISSLIIGGNITSPYIGREANQEPFRFTNGPV 360
DB 301 FDILNNLIFIDWFSVGRNFGYGHVLISSLIIGGNITSPYIGREANQEPFRFTNGPV 360
QY 361 FRTLSIPTLRLLQOPCORHHFNLRGEGVEFSTPTNSFYRGRGTVDLSITELPEDNSVP 420

Db 361 FRTLSIPTLRLLQOPCORHHFNLRGEGVEFSTPTNSFYRGRGTVDLSITELPEDNSVP 420
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Db 421 PREGYSHRLCHATFVQSRGTPFLTTGTVFVSWTHRSATLNTIDPERINQIPLVKGRVWG 480
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Db 481 GTSVITGPGFTGGDILRRNTFGDFVSLQVNNINSPIQRYLRFRYASSRDARVIVLTGAA 540
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Db 541 STGVGGOVSVNMPLOKMEIGENLTSTRTFRYDFSNPFSFRANPDIIIGISEQPLFGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLBRAKANNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
Db 601 SSGELYDKIEIILADATFEASDLBRAKANNALFTSSNOIGLKTDTVDYHIDQVSNLV 660
QY 661 DCLSEDFCLDEKRELSEKVKHAKLSDERNLLQDNFRGINRQDRGWRGSTDITIQGD 720
Db 661 DCLSEDFCLDEKRELSEKVKHAKLSDERNLLQDNFRGINRQDRGWRGSTDITIQGD 720
QY 721 DVPKENVTLPGTVDECYPTLYOKIDESKLYKAYTRYELRGYIIESQDLEIYLIAINAKH 780
Db 721 DVPKENVTLPGTVDECYPTLYOKIDESKLYKAYTRYELRGYIIESQDLEIYLIAINAKH 780
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Db 781 EIVNVPGTGSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

Search completed: October 9, 2003, 13:27:36
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 13:11:09 ; Search time 96 Seconds
(without alignments)
1518.976 Million cell updates/sec

Title: US-09-918-485-2
Perfect score: 4358
Sequence: 1 MEENNOQIPYNCLNPEE.....GPNRCAPHLEWNPDLDCSC 823

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4348	99.8	823	9 AAP80972	Sequence encoded b
2	4339	99.6	823	9 AAP81502	delta-endotoxin ag
3	4294	98.5	1189	12 AAR10130	Lepidopteran-activ
4	4289	98.4	1189	12 AAR10193	Insecticidal cryst
5	4289	98.4	1189	16 AAR71463	Crystall protein en
6	4289	98.4	1189	19 AAW61340	A mutated CryIC pr
7	4289	98.4	1189	20 AAY17793	B. thuringiensis c
8	4289	98.4	1189	21 AAY82401	Bacillus thuringie
9	4289	98.4	1189	23 AAE26465	Bacillus thuringie

10	4289	98.4	1189	23 ABG93819	B. thuringiensis C
11	4288	98.4	1189	14 AAR39757	Delta endotoxin.
12	4288	98.4	1189	19 AAW61337	A mutated CryIC pr
13	4288	98.4	1189	19 AAW61335	A mutated CryIC pr
14	4288	98.4	1189	20 AAY17790	B. thuringiensis c
15	4288	98.4	1189	20 AAY17788	B. thuringiensis c
16	4288	98.4	1189	21 AAY82396	Bacillus thuringie
17	4288	98.4	1189	21 AAY82398	Bacillus thuringie
18	4288	98.4	1189	23 AAE26460	Bacillus thuringie
19	4288	98.4	1189	23 AAE26462	Bacillus thuringie
20	4288	98.4	1189	23 ABG93814	B. thuringiensis C
21	4288	98.4	1189	23 ABG93816	B. thuringiensis C
22	4287	98.4	1189	19 AAW61336	A mutated CryIC pr
23	4287	98.4	1189	20 AAY17789	B. thuringiensis c
24	4287	98.4	1189	21 AAY82397	Bacillus thuringie
25	4287	98.4	1189	23 AAE26461	Bacillus thuringie
26	4287	98.4	1189	23 ABG93815	B. thuringiensis C
27	4283	98.3	1189	19 AAW61339	A mutated CryIC pr
28	4283	98.3	1189	20 AAY17792	B. thuringiensis c
29	4283	98.3	1189	21 AAY82400	Bacillus thuringie
30	4283	98.3	1189	23 AAE26464	Bacillus thuringie
31	4283	98.3	1189	23 ABG93818	B. thuringiensis C
32	4282	98.3	1189	19 AAW61338	A mutated CryIC pr
33	4282	98.3	1189	19 AAW61345	A mutated CryIC pr
34	4282	98.3	1189	20 AAY17791	B. thuringiensis c
35	4282	98.3	1189	20 AAY17783	EG12111 crystal pr
36	4282	98.3	1189	21 AAY82399	Bacillus thuringie
37	4282	98.3	1189	21 AAY82431	Bacillus thuringie
38	4282	98.3	1189	23 AAE26463	Bacillus thuringie
39	4282	98.3	1189	23 AAE26471	Bacillus thuringie
40	4282	98.3	1189	23 ABG93817	B. thuringiensis C
41	4282	98.3	1189	23 ABG93849	B. thuringiensis C
42	4281	98.2	1189	19 AAW61346	A mutated CryIC pr
43	4281	98.2	1189	20 AAY17784	EG12121 crystal pr
44	4281	98.2	1189	21 AAY82432	Bacillus thuringie
45	4281	98.2	1189	23 AAE26472	Bacillus thuringie

ALIGNMENTS

RESULT 1
AAP80972
ID AAP80972 standard; protein; 823 AA.
XX
AC AAP80972;
XX
DT 25-MAR-2003 (updated)
DT 30-OCT-1990 (first entry)
XX
DE Sequence encoded by 3kb Hind III-Pst I fragment of Bacillus
DE thuringiensis (BT) strain aizawai 7-29 and entomocidus 6-01.
XX
KW Microbial insecticide; pesticide; bacterium; Noctuellae;
KW Spodoptera littoralis; Mammetra brassicae.
OS Bacillus thuringiensis.
XX
PN EP295156-A.
XX
PD 14-DEC-1988.
XX
PF 06-MAY-1988; 88EP-0401121.
XX
PR 10-JUN-1987; 87FR-0008090.
XX
(INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Sanchis V, Lereclus D, Menou G, Lecadet MM, Martouret D, Dedonder R;
XX WPI; 1988-355565/50.
DR

XX New DNA sequences encoding insecticidal polypeptide -
PT with specific activity against lepidoptera larvae esp.
PT Spodoptera littoralis
XX
XX Claim 14; Pages 27-29; 37pp; French.
XX
XX It is at least part of the N-terminal region of a polypeptide which is
XX specifically toxic for lepidopteran larvae of the family Noctuellae
XX (esp. Spodoptera littoralis). The DNA encoding it can be incorporated
XX directly in plants or micro-organisms, pref. Pseudomonas, Azospirillum
XX or Rhizobium, which live in the plant environment.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 823 AA;
XX
Query Match 99.8%; Score 4348; DB 9; Length 823;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MEENNQCIPYNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNQCIPYNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Qy 121 NNPATRTRVIDRFRILDLGLERDIPSPRISGFVPLLSVYQAANLHLAILRDSVIFGER 180
Db 121 NNPATRTRVIDRFRILDLGLERDIPSPRISGFVPLLSVYQAANLHLAILRDSVIFGER 180
Qy 181 WGLITINVENYRLRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVL 240
Db 181 WGLITINVENYRLRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVL 240
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Db 241 DTAAPFNYDRYPTOPVQGLTREVYTDPLINPQLOSLVAQLPTFNWESSAIENPHL 300
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Db 301 FOILNLTFTDPSVGRNPFYGGHVRVSSLIIGGNITSPYGRANQEPFRFTNGVP 360
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Db 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFTSTFTYRGRTVDSLTLPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQSGTPELTGTVVFWSTHRSATLNTIDPERINQIPLVKGFVWG 480
Db 421 PREGYSHRLCHATFVQSGTPELTGTVVFWSTHRSATLNTIDPERINQIPLVKGFVWG 480
Qy 481 GTSVITGPGFTGGDILRRNTFGDVSQVNSINSPITQRYRLFRFYASSRDARVILTGAA 540
Db 481 GTSVITGPGFTGGDILRRNTFGDVSQVNSINSPITQRYRLFRFYASSRDARVILTGAA 540
Qy 541 STGVGQGVSNMPLQKTMEIGENLTSRTFRYTDPSNPFSGFRANPDIIIGISQPLFAGSI 600
Db 541 STGVGQGVSNMPLQKTMEIGENLTSRTFRYTDPSNPFSGFRANPDIIIGISQPLFAGSI 600
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Db 601 SSGEYVYDKIEIILADATFEASDLERAKAVNALFTSSNOIGLKTVDYHIDQVSNLV 660
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Db 661 DCLSEBFLDKRELSEKVKHKLSDERNLLQDPNFRGNQPPDRGWSGTDITIQGGD 720
Qy 721 DVFKNYVTLGTVDECPYLYOKIDESKLYKATRYELRGVIEDSOLEYLIAYNAKH 780
Db 721 DVFKNYVTLGTVDECPYLYOKIDESKLYKATRYELRGVIEDSOLEYLIAYNAKH 780
Qy 781 EIVNVPGTGSMLWPLSAQSPIGKCGEPRNCAPHLEWNPDLDCSC 823

Db 781 EIVNVPGTGSMLWPLSAQSPIGKCGEPRNCAPHLEWNPDLDCSC 823
RESULT 2
AAP81502
ID AAP81502 standard; protein; 823 AA.
XX
XX AAP81502;
AC AC
XX 25-MAR-2003 (updated)
DT 23-OCT-1990 (first entry)
XX
XX delta-endotoxin against Lepidoptera larvae.
DB
XX Lepidoptera larvae; insecticide; Bacillus thuringiensis;
KW Spodoptera littoralis; delta endotoxin; 88.
XX
XX synthetic.
OS
XX Key Location/Qualifiers
FH 1..620
FT Region
FT /label=N-terminal half
FT /note="responsible for toxicity"
XX
XX WO8809812-A.
XX
XX 15-DEC-1988.
PD
XX 09-JUN-1988; 88WO-FR00292.
XX
XX 10-JUN-1987; 87FR-0008090.
PR
XX 06-MAY-1988; 88EP-0401121.
PR
XX (INSP) INST PASTEUR.
PA (INSP) INST NAT RECH AGRONOMIQ.
PA
XX Sanchis V, Lereclus D, Menou G;
XX
XX WPI; 1988-368627/51.
XX
XX N-PSDB; AAN81949.
XX
XX New nucleotide sequences encoding new polypeptide -
PT with selective action against lepidopteran larvae esp Spodoptera
PT littoralis
XX
XX Claim 14; Page 52; 65pp; French.
PS
XX Polypeptide is encoded by a 3kb HindIII-PstI fragment of
CC Bacillus thuringiensis. Recombinant sequences can also be
CC constructed from 2 diff strains of B.thuringiensis. The sequence
CC between bases 50 to 985 is claimed separately as this encodes "at
CC least a part of the N-terminal region of an insecticidal
CC polypeptide". There is a variable amino acid at posn 124 which is
CC Ala in the sequence given here but which is Glu in the shorter
CC sequence.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
CC (Updated on 25-MAR-2003 to correct DR field.)
XX
XX Sequence 823 AA;
XX
Query Match 99.6%; Score 4339; DB 9; Length 823;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MEENNQCIPYNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNQCIPYNCLSNPEVLLDGERISTGNSSIDISLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAALANLEGLGNFNFIYVEAFKEWEDP 120

QY 121 NNPATRTRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHLAIRDLSVIFGR 180
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 QY 241 DIAAFFPNYNNRRYPIQPVQQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 DB 241 DIAAFFPNYNNRRYPIQPVQQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 QY 301 FDLNNLTITFDWFSVGRNFWGCHRVISSLIGGNITSPYIGREANQBPSPRFTNGPV 360
 DB 301 FDLNNLTITFDWFSVGRNFWGCHRVISSLIGGNITSPYIGREANQBPSPRFTNGPV 360
 QY 361 FRLTSLPTLLQOPCORHHFNLRGGEGVEFSTPTNSFTYRGRGTVDLSLTELPEPNSVP 420
 DB 361 FRLTSLPTLLQOPCORHHFNLRGGEGVEFSTPTNSFTYRGRGTVDLSLTELPEPNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPELTITGVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 DB 421 PREGYSHRLCHATFVQSGTPELTITGVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYRLRPRYASSRDARVILTGAA 540
 DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYRLRPRYASSRDARVILTGAA 540
 QY 541 STGVGGQSVNMPLOKTMETGENLTSTRTRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
 DB 541 STGVGGQSVNMPLOKTMETGENLTSTRTRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
 QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYDIDQVSNLV 660
 DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYDIDQVSNLV 660
 QY 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDTITIQGSD 720
 DB 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDTITIQGSD 720
 QY 721 DVPKENVTLPGTVDECYPTLYOKIDESKIKAYTRYELRGYIEDSQDLEIYLIAYNAXH 780
 DB 721 DVPKENVTLPGTVDECYPTLYOKIDESKIKAYTRYELRGYIEDSQDLEIYLIAYNAXH 780
 QY 781 EIVNVPETGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPETGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 3

AAR10130
 ID AAR10130 standard; Protein; 1189 AA.

XX AAR10130;

XX AC

XX 25-MAR-2003 (updated)

DT 20-MAR-1991 (first entry)

XX XX

DE Lepidopteran-active toxin C.

XX XX

KW Lepidopteran-active toxin C; pest control.

XX XX

OS Bacillus thuringiensis PS81L (NRRL B-18484).

XX XX

PN EP405810-A.

XX XX

PD 02-JAN-1991.

XX XX

PF 18-JUN-1990; 90EP-0306594.

XX XX

PR 14-DEC-1989; 89US-0451261.

PR 27-JUN-1989; 89US-0371955.

XX (MYCO) MYCOGEN CORP.
 PA Payne J, Sick AJ;
 XX WPI; 1991-009132/02.
 DR N-PSDB; AAQ10181.
 DR XX
 PT Bacillus thuringiensis contg. DNA encoding lepidopteran-active
 toxin - use of microorganisms transformed with the toxin gene
 in pest control
 PT
 XX Claim 5; Page 19-23; 28pp; English.
 PS
 XX Expression of the toxin gene by a host results, directly or
 CC indirectly, in the intracellular prodn. and maintenance of the
 CC pesticide.
 CC See also AAQ10179-82.
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1189 AA;

Query Match 98.5%; Score 4294; DB 12; Length 1189;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 815; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MEENNQCIPYNCLSNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPYNCLSNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFWGIVGSPQWDAFLVQIEQLINERIAEFARNAAIANLEGIGNNFNIYVEAFKEWEEP 120
 DB 61 DFWGIVGSPQWDAFLVQIEQLINERIAEFARNAAIANLEGIGNNFNIYVEAFKEWEEP 120
 QY 121 NNPATRTRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHLAIRDLSVIFGR 180
 DB 121 NNPATRTRVDRFRILDLGLLDRIPSPRISGFEVPLLSVYAAQANLHLAIRDLSVIFGR 180
 QY 181 WGLTTNNVNNYNNRLRHIDEYADHCANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
 DB 181 WGLTTNNVNNYNNRLRHIDEYADHCANTYNGLNLPKSTYQDWITYNRLRDLTLTVL 240
 QY 241 DIAAFFPNYNNRRYPIQPVQQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 DB 241 DIAAFFPNYNNRRYPIQPVQQLTRVYTDPLINFNPQLQSVQALPTFNVMSSAIRNPHL 300
 QY 301 FDLNNLTITFDWFSVGRNFWGCHRVISSLIGGNITSPYIGREANQBPSPRFTNGPV 360
 DB 301 FDLNNLTITFDWFSVGRNFWGCHRVISSLIGGNITSPYIGREANQBPSPRFTNGPV 360
 QY 361 FRLTSLPTLLQOPCORHHFNLRGGEGVEFSTPTNSFTYRGRGTVDLSLTELPEPNSVP 420
 DB 361 FRLTSLPTLLQOPCORHHFNLRGGEGVEFSTPTNSFTYRGRGTVDLSLTELPEPNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPELTITGVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 DB 421 PREGYSHRLCHATFVQSGTPELTITGVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYRLRPRYASSRDARVILTGAA 540
 DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYRLRPRYASSRDARVILTGAA 540
 QY 541 STGVGGQSVNMPLOKTMETGENLTSTRTRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
 DB 541 STGVGGQSVNMPLOKTMETGENLTSTRTRYTDPSNPFSPRANPDIIGISEQPLFGAGSI 600
 QY 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYDIDQVSNLV 660
 DB 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTVDYDIDQVSNLV 660
 QY 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDTITIQGSD 720
 DB 661 DCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGSGTDTITIQGSD 720

QY	721	DVFKENYVTLPGTVDECYPTLYQKIDESKAYTRYELRGYIEDSDLEIYLIAVNAKH	780			
Db	721	DVFKENYVTLPGTVDECYPTLYQKIDESKAYTRYELRGYIEDSDLEIYLIRYNAKH	780			
QY	781	EIVNVPGTSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC	823			
Db	781	EIVNVPGTSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC	823			
RESULT 4						
AA	10193	standard; Protein; 1189 AA.				
AC	10193;					
XX	25-MAR-2003	(updated)				
DT	27-MAR-1991	(first entry)				
XX	Insecticidal crystal protein (ICP) entomocidus HD-110 of gene bt4.					
XX	Insecticide; Lepidoptera; Coleoptera.					
XX	Bacillus thuringiensis.					
OS	EP408403-A.					
XX	16-JAN-1991.					
XX	29-MAY-1990;	90EP-0401427.				
XX	29-MAY-1990;	90EP-0401427.				
PR	31-MAY-1989;	89EP-0401499.				
XX	(PLBZ) PLANT GENETICS SYSTEMS NV..					
PA	Vanmellaer H, Botterman J, Vanrie J, Joos H;					
PI	WPI; 1991-016587/03.					
DR	N-PSDB; AAQ10229.					
XX	Insect-resistant transgenic plant cells - transformed with genes					
PI	encoding different non-competitively binding Bacillus					
PI	thuringiensis insecticidal proteins					
XX	Disclosure; Fig 14; 82pp; English.					
PS	Sequence encoding the protein may be used in transformation of crop					
CC	plants, providing resistance to insect (esp. lepidoptera and Coleoptera)					
CC	attack, without resort to insecticides which incur problems with					
CC	development of insect resistance.					
CC	(Updated on 25-MAR-2003 to correct PA field.)					
CC	(Updated on 25-MAR-2003 to correct PI field.)					
XX	Sequence 1189 AA;					
Query Match						
Best Local Similarity 98.4%; Score 4289; DB 12; Length 1189;						
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;						
QY	1	MEENNQCIPYNCISNPBVLIDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI	60			
Db	1	MEENNQCIPYNCISNPBVLIDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI	60			
QY	61	DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAANLEGLGNFNFIYVEAFKEWEDP	120			
Db	61	DFWVGIVGPSQWDAFLVQIEQLINERIAEFARNAANLEGLGNFNFIYVEAFKEWEDP	120			
QY	121	NNPATRVRIDRFRILDLGLERDIPSRISGFEVPLLSVYAQAANLHAILRDSVIFGER	180			
Db	121	NNPATRVRIDRFRILDLGLERDIPSRISGFEVPLLSVYAQAANLHAILRDSVIFGER	180			
QY	181	WGLTTNNVNNYELRIHIDEYADHCANTYNNGLNLPKSYQDMITYNLRDRDLTLVL	240			

DR WPI; 1995-115446/15.
XX N-PSDB; AAQ80646.
PT New Bacillus thuringiensis hybrid toxin fragment - derived from
PT two different cry proteins, and related hybrid toxins.
PT recombinant DNA, vectors, transformed plants and microorganisms,
PT for insect control.
XX
PS Disclosure; Page 18-23; 65pp; English.
XX
CC Crystal proteins CryIC, CryIE and CryIA are toxic to lepidopterans.
CC CryIC is particularly active against *S. exigua* and *M. brassicae*.
CC Toxic fragments of crystal proteins are thought to be composed of
CC three distinct structural domains. Domain I, the most N-terminal
CC domain, consists of 7 alpha-helices. Domain II comprises 3 beta-
CC sheets and domain III (the most C-terminal) folds into a beta-
CC sandwich. If projected onto CryI sequences, domain I runs from about
CC AA residue 28-260, domain II from about 260-460 and domain III from
CC about 460-600.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1189 AA;
Query Match 98.4%; Score 4289; DB 16; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 MEENNQNCIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQNCIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
DB 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120
QY 121 NNPATRTRVDRFRILDLGLERDIPSRISGFEVPLLSVYAAQANHLAILRDSVIFGER 180
DB 121 NNPATRTRVDRFRILDLGLERDIPSRISGFEVPLLSVYAAQANHLAILRDSVIFGER 180
QY 181 WGLTTINVENYNLRIHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
DB 181 WGLTTINVENYNLRIHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
QY 241 DIAAFFPNYDNRYPQVQGLTREVTYDPLINFNPQLOQVAQLPTFNVMESSAIRNPHL 300
DB 241 DIAAFFPNYDNRYPQVQGLTREVTYDPLINFNPQLOQVAQLPTFNVMESSAIRNPHL 300
QY 301 FDIILNLTITDFWFSVGRNFWGHRVVISLIGGNITSPYIGREANQEPSPRFTNGPV 360
DB 301 FDIILNLTITDFWFSVGRNFWGHRVVISLIGGNITSPYIGREANQEPSPRFTNGPV 360
QY 361 FRTLSIPTLLAQPCQRHFNLRGGVGFSTPTNSFTYRGRGTVDLSLTLPEDNSVP 420
DB 361 FRTLSIPTLLAQPCQRHFNLRGGVGFSTPTNSFTYRGRGTVDLSLTLPEDNSVP 420
QY 421 PREGYSHRLCHATFVQSGTFPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVWG 480
DB 421 PREGYSHRLCHATFVQSGTFPFLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFVWG 480
QY 481 GTSVITGPGTGGDILRRNTFGFVSLQVNNINSPIQRYVLRPRYASSRDARVILTGAA 540
DB 481 GTSVITGPGTGGDILRRNTFGFVSLQVNNINSPIQRYVLRPRYASSRDARVILTGAA 540
QY 541 STVGGOVSNNMPLQKTMETGENLTSTRTRYTDFSNPESFRANPDIIIGISEQPLFAGSI 600
DB 541 STVGGOVSNNMPLQKTMETGENLTSTRTRYTDFSNPESFRANPDIIIGISEQPLFAGSI 600
QY 601 SSGELYDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYDHDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDYDHDQVSNLV 660
QY 661 DCLSDSEFCDEKRELSKVHAKRLSDERNLLQDPNFRGINRQDRGWRGSTDTITQGGD 720

DB 661 DCLSDSEFCDEKRELSKVHAKRLSDERNLLQDPNFRGINRQDRGWRGSTDTITQGGD 720
QY 721 DVFKEKNVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSDLEIYLIYNAKH 780
DB 721 DVFKEKNVTLPGTVDECYPTLYQKIDESKLYATRYELRGYIEDSDLEIYLIYNAKH 780
QY 781 EIVNVFGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVFGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
RESULT 6
AAW61340
ID AAW61340 standard; Protein; 1189 AA.
XX
AC AAW61340;
XX
DT 30-SEP-1998 (first entry)
XX
DE
XX
KW Mutant; CryIC delta-endotoxin; CryIC.579; insecticidal activity;
KW control; insect; lepidoptera; Spodoptera exigua; Plutella xylostella;
KW trichoplusia ni; Spodoptera frugiperda.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Misc-difference 121 /label= N121H
FT
XX WO9823641-A1.
XX
XX 04-JUN-1998.
XX
XX 26-NOV-1997; 97WO-US22181.
XX
XX 27-NOV-1996; 96US-0757536.
XX
XX (ECOG-) ECOGEN INC.
XX
PI Baum JA, Gilmer AJ, Mettus A;
XX
DR WPI; 1998-322660/28.
DR N-PSDB; AAV27848.
XX
XX New Bacillus thuringiensis nucleic acid segments - comprising
PT delta-endotoxin gene fragments, used for the control of insects,
PT particularly Lepidopteran pests
XX
PS Claim 1; Pages 124-126; 270pp; English.
XX
CC The present sequence represents a mutant of the CryIC delta-endotoxin
CC of Bacillus thuringiensis designated CryIC.499, where the Asn at
CC position 121 of the wild type CryIC protein is substituted with His.
CC The protein shows insecticidal activity, and can be sprayed onto
CC plants or expressed in transgenic plants for the control of insects,
CC particularly lepidopteran pests such as Spodoptera exigua, Plutella
CC xylostella, Trichoplusia ni and Spodoptera frugiperda.
XX
SQ Sequence 1189 AA;
Query Match 98.4%; Score 4289; DB 19; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 1 MEENNQNCIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
DB 1 MEENNQNCIPYNCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
QY 61 DFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKEWEDP 120

Db 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAALNLEGLGNFNFIYVEAFKEWEDP 120
Qy 121 NNPATRVDRFRILDLGLERDIPSPRISGFEVPLLSVYQAQANLHAILRDSVIFGR 180
Db 121 HNPATRVDRFRILDLGLERDIPSPRISGFEVPLLSVYQAQANLHAILRDSVIFGR 180
Qy 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAFFPNYNNRYPIQPVGQLTREVTYDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYNNRYPIQPVGQLTREVTYDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTFTDWFSGVGRNFWGGRHVRVSSILIGGNITSPYIGREANQPPRSFTNGPV 360
Db 301 FDILNNLTFTDWFSGVGRNFWGGRHVRVSSILIGGNITSPYIGREANQPPRSFTNGPV 360
Qy 361 FRTLSTPLRLLQOPCORHFNLRGEGVEFSTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Db 361 FRTLSTPLRLLQOPWPAPPFNLRGEGVEFSTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQVSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
Db 421 PREGYSHRLCHATFVQVSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYELRFRYASRRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYELRFRYASRRDARVILTGAA 540
Qy 541 STGVGGQVNMPLQKTMIEGNTSRFTYDFSNPFSFRANPDIIIGISEOPLGAGSI 600
Db 541 STGVGGQVNMPLQKTMIEGNTSRFTYDFSNPFSFRANPDIIIGISEOPLGAGSI 600
Qy 601 SSGELYIDKIEIILADATFEASDLERAKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAKAVNALFTSSNQIGLKTVDYHIDQVSNLV 660
Qy 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFRGINQPPRGWRGSDTITIQGSD 720
Db 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFRGINQPPRGWRGSDTITIQGSD 720
Qy 721 DVFKENYVTLGTVDECYPTLYQKIDESKIKAYTRYELRGYIEDSQDLEIYLIYRNAXH 780
Db 721 DVFKENYVTLGTVDECYPTLYQKIDESKIKAYTRYELRGYIEDSQDLEIYLIYRNAXH 780
Qy 781 EIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

RESULT 7

AY17793
ID AY17793 standard; Protein; 1189 AA.
XX AC AY17793;
XT 12-AUG-1999 (first entry)
XX DE B. thuringiensis crystal protein CryIC.499 protein sequence.
XX KW Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;
KW lepidopteran insect; CryIC; genetic engineering; mucagenesis; mutant;
KW caterpillar; beetle; mosquito; toxic; modification.
XX OS Bacillus thuringiensis.
OS Synthetic.
XX US5914318-A.
XX 22-JUN-1999.
XX 26-NOV-1997; 97US-0980071.

XX 26-NOV-1997; 97US-0980071.
PR 27-NOV-1996; 96US-0757536.
XX (ECOG-) ECOGEN INC.
XX Baum JA, Gilmer AJ, Mettuss AL;
XX WPI: 1999-370510/31.
DR N-PSDB; AAX80039.
XX New modified delta-endotoxin crystal proteins from Bacillus
PT thuringiensis are useful in insecticidal compositions
XX Example 13; Column 94-97; 144pp; English.
XX The present invention describes a new composition comprising an isolated
CC polypeptide for modified Bacillus thuringiensis crystal proteins (CryIC).
CC The polypeptide of the composition is insecticidally-active against
CC Lepidoptera. The composition is toxic to an insect cell and comprised
CC within an insecticidal formulation can be used as a plant protective
CC spray which is toxic to caterpillars, beetles and mosquitoes. The
CC polypeptide of the composition may be used to kill an insect through
CC ingestion of the composition directly or by ingestion of a plant coated
CC with the composition or a transgenic plant that expresses the polypeptide
CC composition. The insecticidal proteins produced by B. thuringiensis are
CC harmless to plants and other non-targeted organisms but toxic to their
CC specific target insect. The polypeptides have improved toxicity so a
CC reduced amount of bioinsecticide per unit area of treated crop can be
CC used allowing economic and efficient utilization in the field. The
CC present sequence represents a modified B. thuringiensis crystal protein.
XX Sequence 1189 AA;
SQ
Query Match 98.4%; Score 4289; DB 20; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
Qy 1 MEENQNCIPTNCLSNPEEVLDERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENQNCIPTNCLSNPEEVLDERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Qy 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAALNLEGLGNFNFIYVEAFKEWEDP 120
Db 61 DFVWGVGSQWDAFLVQIEQLINERIAEPARNAALNLEGLGNFNFIYVEAFKEWEDP 120
Qy 121 NNPATRVDRFRILDLGLERDIPSPRISGFEVPLLSVYQAQANLHAILRDSVIFGR 180
Db 121 NNPATRVDRFRILDLGLERDIPSPRISGFEVPLLSVYQAQANLHAILRDSVIFGR 180
Qy 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLTVL 240
Db 181 WGLTTINVENYNNRLIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLTVL 240
Qy 241 DIAAFFPNYNNRYPIQPVGQLTREVTYDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
Db 241 DIAAFFPNYNNRYPIQPVGQLTREVTYDPLINFPQLQSVQALPTFNWESSAIRNPHL 300
Qy 301 FDILNNLTFTDWFSGVGRNFWGGRHVRVSSILIGGNITSPYIGREANQPPRSFTNGPV 360
Db 301 FDILNNLTFTDWFSGVGRNFWGGRHVRVSSILIGGNITSPYIGREANQPPRSFTNGPV 360
Qy 361 FRTLSTPLRLLQOPCORHFNLRGEGVEFSTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Db 361 FRTLSTPLRLLQOPWPAPPFNLRGEGVEFSTPTNSFTYGRGRTVDSLTLPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQVSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
Db 421 PREGYSHRLCHATFVQVSGTPELTITGVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYELRFRYASRRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNNINSPIQRYELRFRYASRRDARVILTGAA 540

KW Cry1 protein; delta-endotoxin; insect resistance; lepidopteran insect;
XX transgenic plant; transgenic; mutant; mutein.
OS Bacillus thuringiensis.
OS Synthetic.
XX US6313378-B1.
XX 06-NOV-2001.
XX 21-JUN-1999; 99US-0337635.
XX 26-NOV-1997; 97US-0980071.
XX 27-NOV-1996; 96US-0757536.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX Baum JA, Gilmer AJ, Mettus AL;
XX WPI; 2002-033341/04.
XX N-PSDB; AAD44215.
XX Transgenic plants, comprises nucleic acid encoding Cry1C
XX delta-endotoxin polypeptide, has improved resistance to Lepidopteran
XX insects
XX
XX Disclosure; Column 209-216; 151pp; English.
XX
XX The present invention relates to novel transgenic plants comprising Cry1
XX delta-endotoxin genes, in particular cry1C genes that encode modified
XX crystal proteins having improved resistance to Lepidopteran insects. The
XX plants that express the mutated Cry1C delta-endotoxin crystal proteins
XX are noncoryledonous (corn, wheat, oat, rice, barley, turf grass, pasture
XX grass) or dicotyledonous (legume, soybean, cotton, fruit, berry, tree).
XX The present sequence is Bacillus thuringiensis Cry1C.499 mutant protein.
XX
XX Sequence 1189 AA;
SQ

Query Match 88.4%; Score 4289; DB 23; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MEENNQCIPYNCNPNBEVLDDGERISTGNSIDISLSVQLVSNFVGGFLVGLI 60
DB 1 MEENNQCIPYNCNPNBEVLDDGERISTGNSIDISLSVQLVSNFVGGFLVGLI 60
QY 61 DFVWGIVGSPQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEEDP 120
DB 61 DFVWGIVGSPQWDAFLVQIEQLINERIAEFARNAATANLEGLGNFNFIYVEAFKEWEEDP 120
QY 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFVEPLLSVYQAANLHLAILRDSVIFGER 180
DB 121 NNPATRTRVIDRFRILDGLLERDIPSPRISGFVEPLLSVYQAANLHLAILRDSVIFGER 180
QY 181 WGLTTINVENYNRLIRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVL 240
DB 181 WGLTTINVENYNRLIRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVL 240
QY 241 DIAAFPPNDRRYPIQVQOLTRVYTDPLINFPOLQSVQAQLTFNVMESSAIRNPHL 300
DB 241 DIAAFPPNDRRYPIQVQOLTRVYTDPLINFPOLQSVQAQLTFNVMESSAIRNPHL 300
QY 301 FDLIANNLITFDWFSVGRNPFYMGCHRVISLLIGCGNITSPYIGREANQEPSPRSTFNGPV 360
DB 301 FDLIANNLITFDWFSVGRNPFYMGCHRVISLLIGCGNITSPYIGREANQEPSPRSTFNGPV 360
QY 361 FRLTSLPTLRLLOQPCORHHNLRGEGVEFTPTNSFTYRGVGTVDLSLTPEDNSVP 420
DB 361 FRLTSLPTLRLLOQPCORHHNLRGEGVEFTPTNSFTYRGVGTVDLSLTPEDNSVP 420
QY 421 PREGSHRLCHATVQVRSQTPPLTGVFVSWTHRSATLNTWIDPERINQIPLVKGFRVWG 480
DB 421 PREGSHRLCHATVQVRSQTPPLTGVFVSWTHRSATLNTWIDPERINQIPLVKGFRVWG 480

QY 481 GTSVITGPGTGGDILRENTPGDFVSLQVNNINSPTQRYRLFRFYASSRDARVIVLTGAA 540
DB 481 GTSVITGPGTGGDILRENTPGDFVSLQVNNINSPTQRYRLFRFYASSRDARVIVLTGAA 540
QY 541 STVGQGVSNMPLQKTMEIGENLTSTRFTYDFSNPESFRANPDIIGISEQPLFGAGSI 600
DB 541 STVGQGVSNMPLQKTMEIGENLTSTRFTYDFSNPESFRANPDIIGISEQPLFGAGSI 600
QY 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTDTVTDYHIDQVSNLV 660
DB 601 SSGELYDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLKTDTVTDYHIDQVSNLV 660
QY 661 DCLSDREFCLDEKRELSKVKHAKLSDERNLLQDENFRGINRQPDGRWGSGTDITIQGSD 720
DB 661 DCLSDREFCLDEKRELSKVKHAKLSDERNLLQDENFRGINRQPDGRWGSGTDITIQGSD 720
QY 721 DVFKENYVTLPGTVDECTPTLYOKIDESKLYATRYELRGYIEDSQDLIYLIAVNAKH 780
DB 721 DVFKENYVTLPGTVDECTPTLYOKIDESKLYATRYELRGYIEDSQDLIYLIAVNAKH 780
QY 781 EIVNVPQTGSLMPLSAQSPICGCEPNRCAPHLEWNPDLDCSC 823
DB 781 EIVNVPQTGSLMPLSAQSPICGCEPNRCAPHLEWNPDLDCSC 823

RESULT 10
ABG93819
ID ABG93819 standard; Protein; 1189 AA.
XX
XX AC ABG93819;
XX 26-NOV-2002 (first entry)
XX B. thuringiensis Cry mutant Cry1C-H121H.
XX Crystal protein; Cry1C; mutant; delta-endotoxin; insecticide; mutein;
XX lepidopteran insect.
XX Bacillus thuringiensis.
XX Synthetic.
XX US6423828-B1.
XX 23-JUL-2002.
XX 22-JUN-1999; 99US-0337280.
XX 26-NOV-1997; 97US-0980071.
XX 27-NOV-1996; 96US-0757536.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX Baum JA, Gilmer AJ, Mettus AL;
XX WPI; 2002-705183/76.
XX DR N-PSDB; ABS70786.
XX
XX New delta endotoxin polypeptides, which are Lepidopteran-toxic
XX polypeptides, useful as an insecticide, particularly for killing
XX Lepidopteran insects or insect cells -
XX
XX Example 6; Column 101-106; 149pp; English.
XX
XX The invention relates to an isolated Cry1Ca* delta-endotoxin polypeptide
XX useful as an insecticide. Cry is a crystal protein from B. thuringiensis.
XX The isolated Cry1Ca* delta-endotoxin polypeptide comprises:
XX (a) one or more amino acid mutations in the loop regions between alpha
XX helices 4 and 5 of domain 1; (b) one or more amino acid mutations in the
XX loop region between alpha helices 6 and 7 of domain 1; or (c) has
XX improved activity against Lepidopteran insects relative to a native Cry1C
XX delta-endotoxin polypeptide. The Cry1Ca* delta-endotoxin polypeptide is
XX useful as an insecticide, particularly for killing Lepidopteran insects

CC or insect cells. The present sequence represents a mutant CryIC protein
 CC of the invention.

XX SQ Sequence 1189 AA;
 Query Match 98.4%; Score 4289; DB 23; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVWGIQVGSQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFIYVEAFKWEEDP 120
 DB 61 DFVWGIQVGSQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFIYVEAFKWEEDP 120
 QY 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYQAANLHLAIRDSDVIFGER 180
 DB 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYQAANLHLAIRDSDVIFGER 180
 QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITTYNLRDLTLTVL 240
 DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITTYNLRDLTLTVL 240
 QY 241 DIAAFPNDNRRYPQIPVQQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300
 DB 241 DIAAFPNDNRRYPQIPVQQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300
 QY 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLLGGNITSPIYGREANQPPRSFTFNGVP 360
 DB 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLLGGNITSPIYGREANQPPRSFTFNGVP 360
 QY 361 FRTLSTPLRLQLQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 DB 361 FRTLSTPLRLQLQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 DB 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480
 QY 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSIPITQRYRLFRYASSDARVILVTGAA 540
 DB 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSIPITQRYRLFRYASSDARVILVTGAA 540
 QY 541 STGVGQVSVNMPLOKTMETIGENLTSRTRYTDFSNPPSFRANPDIIIGISEQPLFCAGSI 600
 DB 541 STGVGQVSVNMPLOKTMETIGENLTSRTRYTDFSNPPSFRANPDIIIGISEQPLFCAGSI 600
 QY 601 SSGELYIDKIEIILADATPEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
 DB 601 SSGELYIDKIEIILADATPEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
 QY 661 DCLSEFCLEKREISEKVKHAKRLSDERNLLQDNFRGINQPPRGWGSTDIITIQGGD 720
 DB 661 DCLSEFCLEKREISEKVKHAKRLSDERNLLQDNFRGINQPPRGWGSTDIITIQGGD 720
 QY 721 DVFKNYVTLPGTVDECPYLYQKIDESKAYTRYELRGVIEDSQDLIELYLIRYNAKH 780
 DB 721 DVFKNYVTLPGTVDECPYLYQKIDESKAYTRYELRGVIEDSQDLIELYLIRYNAKH 780
 QY 781 EIVNVPGTGLWPLSAQSPIGKGBPNRCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPGTGLWPLSAQSPIGKGBPNRCAPHLEWNPDLDCSC 823

RESULT 11

AAR39757

ID AAR39757 standard; Protein; 1189 AA.

XX AC AAR39757;

XX XX

DT 25-MAR-2003 (updated)

DT 28-JAN-1994 (first entry)
 XX Delta endotoxin.
 XX Endotoxin; Bacillus; lice; insecticide; sheep.
 OS Bacillus thuringiensis PS81I (Clone 81IB2).
 PN W09314641-A1.
 XX W09314641-A1.
 XX 05-AUG-1993.
 PF 31-DEC-1992; 92WO-US11337.
 XX 29-JAN-1992; 92US-0828788.
 XX (MYCO) MYCOGEN CORP.
 XX Hickie LA, Payne J;
 XX WPI; 1993-258266/32.
 DR N-PSDB; AAQ47294.
 PT Controlling biting lice on sheep - comprises administering
 PT Bacillus thuringiensis toxins to host
 PS Disclosure; Page 58-60; 64pp; English.
 XX Many strains of Bacillus thuringiensis (B.t) produce insecticidal
 CC delta endotoxins. A number of these endotoxins have been found to
 CC be toxic to Damilina ovis, the biting louse of sheep. The B.T.
 CC isolates which produce these toxins can be grown and the delta
 CC endotoxin which is produced can be recovered by standard procedures.
 CC The genes encoding these endotoxins can also be transferred to a
 CC suitable host via a recombinant vector and the resulting
 CC transformants used in methods to control lice.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 1189 AA;
 Query Match 98.4%; Score 4288; DB 14; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPNCLSNPEEVLDDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVWGIQVGSQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFIYVEAFKWEEDP 120
 DB 61 DFVWGIQVGSQWDAFLVQIEQLINERIAAFARNAAIANLEGLNPNFIYVEAFKWEEDP 120
 QY 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYQAANLHLAIRDSDVIFGER 180
 DB 121 NNPATRTRVIDRFRILDDGLLDRIDPSFRISGFEVPLLSVYQAANLHLAIRDSDVIFGER 180
 QY 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITTYNLRDLTLTVL 240
 DB 181 WGLTTINVENNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITTYNLRDLTLTVL 240
 QY 241 DIAAFPNDNRRYPQIPVQQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300
 DB 241 DIAAFPNDNRRYPQIPVQQLTREYVTDPLINFNPQLQSVQALPTFNVMESSAIRNPHL 300
 QY 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLLGGNITSPIYGREANQPPRSFTFNGVP 360
 DB 301 FDILNNLTIFTDWSVGRNFGVGGHVRVSSLLGGNITSPIYGREANQPPRSFTFNGVP 360
 QY 361 FRTLSTPLRLQLQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 DB 361 FRTLSTPLRLQLQPCQRHHNLRGEGVEFSTPTNSFTYRGRGTVDSTLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQSGTPTLTTGVVFSWTHRSATLTNTIDPERINQIPLVKGFRVWG 480

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Db 421 PREGSHRLCHATFVQSGTPTLTGGVFSWTHRSATLNTIDPERINQPLVKGFRVWG 480
Qy 481 GTSVITGPGTGGDILRRNTGDFVSLQVNSPITQRYRLRFYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTGDFVSLQVNSPITQRYRLRFYASSRDARVILTGAA 540
Qy 541 STGVGGQVSNMPLQKTMEIGENITSTRTFYTDFSNPFSFRANPDIIIGISEQPLFGAGSI 600
Db 541 STGVGGQVSNMPLQKTMEIGENITSTRTFYTDFSNPFSFRANPDIIIGISEQPLFGAGSI 600
Qy 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
Qy 661 DCLSDPECLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGSTDTITIQGGD 720
Db 661 DCLSDPECLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGSTDTITIQGGD 720
Qy 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKAYTRYELRGYIEDSDLEIYLIYNAKH 780
Db 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKAYTRYELRGYIEDSDLEIYLIYNAKH 780
Qy 781 EIVNVPGTGSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823

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RESULT 12

AAW61337 standard; Protein; 1189 AA.

XX AAW61337;

DT 30-SEP-1998 (first entry)

DE A mutated Cry1C protein designated Cry1C-R180A.

KW Mutant; Cry1C delta-endotoxin; Cry1C-R180A; insecticidal activity;
control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;
Trichoplusia ni; Spodoptera frugiperda.

XX Synthetic.

OS Bacillus thuringiensis.

XX Key Location/Qualifiers

FT Misc-difference 148 /label= R180A

XX WO9823641-A1.

XX 04-JUN-1998.

XX 26-NOV-1997; 97MO-US22181.

XX 27-NOV-1996; 96US-0757536.

XX (ECOG-) ECOGEN INC.

XX Baum JA, Gilmer AJ, Mettus A;

XX WPI; 1998-322660/28.

XX N-PSDB; AAV27845.

XX New Bacillus thuringiensis nucleic acid segments - comprising
delta-endotoxin gene fragments, used for the control of insects,
particularly Lepidopteran pests

XX Claim 1; Pages 120-122; 270pp; English.

XX The present sequence represents a mutant of the Cry1C delta-endotoxin
of Bacillus thuringiensis designated Cry1C-R180A, where the Arg at
position 180 of the wild type Cry1C protein is substituted with Ala.

CC The protein shows insecticidal activity, and can be sprayed onto plants
or expressed in transgenic plants for the control of insects,
particularly Lepidopteran pests such as Spodoptera exigua, Plutella
xylostella, Trichoplusia ni and Spodoptera frugiperda.

XX Sequence 1189 AA;

Qy Query Match 98.4%; Score 4288; DB 19; Length 1189;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MEENNQOCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60
Db 1 MEENNQOCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGLI 60

Qy 61 DFVWGVIPGSDWDAFLVQIQLINERIAEFARNAALANLEGLGNFNIIYVEAFKEEEDP 120
Db 61 DFVWGVIPGSDWDAFLVQIQLINERIAEFARNAALANLEGLGNFNIIYVEAFKEEEDP 120

Qy 121 NNPATRTRVIDRPIILDGLLDERDIPSGRISGPREVPLLSVYAAANLHLAILRDSVIFGER 180
Db 121 NNPATRTRVIDRPIILDGLLDERDIPSGRISGFEVPLLSVYAAANLHLAILRDSVIFGER 180

Qy 181 WGLTTINVENNENLIRHIDEYADHCANTYNRGLANLPKSTVQDWITYNLRDLTLTVL 240
Db 181 WGLTTINVENNENLIRHIDEYADHCANTYNRGLANLPKSTVQDWITYNLRDLTLTVL 240

Qy 241 DIAAFFPNYDNRRIPIQVGGITREVTYDPLINFNQLOSVAQLPTFNVMESAINRPHL 300
Db 241 DIAAFFPNYDNRRIPIQVGGITREVTYDPLINFNQLOSVAQLPTFNVMESAINRPHL 300

Qy 301 FDIILNLTIFTDFSVGRNFWGGRHVISSLIGGNITSPIYGREANQEPFRSFTENGVP 360
Db 301 FDIILNLTIFTDFSVGRNFWGGRHVISSLIGGNITSPIYGREANQEPFRSFTENGVP 360

Qy 361 FRTLSIPTLRLLQPCORHFNLRGEGVEFSTPTNSFTYRGRTVDSLTELPEDNSVP 420
Db 361 FRTLSNPTLRLLQPCWPAPPENLAGVEGVEFSTPTNSFTYRGRTVDSLTELPEDNSVP 420

Qy 421 PREGYSRLCHATFVQSGTPTLTGGVFSWTHRSATLNTIDPERINQPLVKGFRVWG 480
Db 421 PREGYSRLCHATFVQSGTPTLTGGVFSWTHRSATLNTIDPERINQPLVKGFRVWG 480

Qy 481 GTSVITGPGTGGDILRRNTGDFVSLQVNSPITQRYRLRFYASSRDARVILTGAA 540
Db 481 GTSVITGPGTGGDILRRNTGDFVSLQVNSPITQRYRLRFYASSRDARVILTGAA 540

Qy 541 STGVGGQVSNMPLQKTMEIGENITSTRTFYTDFSNPFSFRANPDIIIGISEQPLFGAGSI 600
Db 541 STGVGGQVSNMPLQKTMEIGENITSTRTFYTDFSNPFSFRANPDIIIGISEQPLFGAGSI 600

Qy 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660
Db 601 SSGELYIDKIEIILADATFEASDLERAQKAVNALFTSSNQIGLTKTDVTDYHIDQVSNLV 660

Qy 661 DCLSDPECLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGSTDTITIQGGD 720
Db 661 DCLSDPECLDEKRELSEKVKHAKLSDERNLQDPNFRGINRQPDGRWGSTDTITIQGGD 720

Qy 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKAYTRYELRGYIEDSDLEIYLIYNAKH 780
Db 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKAYTRYELRGYIEDSDLEIYLIYNAKH 780

Qy 781 EIVNVPGTGSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823
Db 781 EIVNVPGTGSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSC 823

RESULT 13
AAW61335
ID AAW61335 standard; Protein; 1189 AA.
XX
XX
AC AAW61335;

XX 30-SEP-1998 (first entry)
 XX A mutated Cry1C protein designated Cry1C-R148A.
 DE Mutant; Cry1C delta-endotoxin; Cry1C-R148A; insecticidal activity;
 XX control; insect; Lepidoptera; Spodoptera exigua; Plutella xylostella;
 KW Trichoplusia ni; Spodoptera frugiperda.
 KW
 XX Synthetic.
 OS Bacillus thuringiensis.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 148
 FT /label= R148A
 FT
 XX WO9823641-A1.
 XX
 XX 04-JUN-1998.
 XX
 XX 26-NOV-1997; 97WO-US22181.
 XX
 XX 27-NOV-1996; 96US-0757536.
 XX
 XX (ECOG-) ECOGEN INC.
 XX
 XX Baum JA, Gilmer AJ, Mettuss A;
 PI WPI; 1998-322660/28.
 XX N-PSDB; AAV27843.
 DR
 XX New Bacillus thuringiensis nucleic acid segments - comprising
 PT delta-endotoxin gene fragments, used for the control of insects,
 PT particularly Lepidopteran pests
 XX
 XX Claim 1; Pages 118-119; 270pp; English.
 PS
 XX The present sequence represents a mutant of the Cry1C delta-endotoxin
 CC of Bacillus thuringiensis designated Cry1C-R148A. The protein shows
 CC insecticidal activity, and can be sprayed onto plants or expressed in
 CC transgenic plants for the control of insects, particularly Lepidopteran
 CC pests such as Spodoptera exigua, Plutella xylostella, Trichoplusia ni
 CC and Spodoptera frugiperda.
 XX
 SQ Sequence 1189 AA;
 Query Match 98.4%; Score 4288; DB 19; Length 1189;
 Best Local Similarity 98.9%; Pred. NO. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MEENNQNCIPYCNLSNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQNCIPYCNLSNPEVLLDGERISTGNSSIDISLSVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVWGVGSQWDAFLVQTEQLINERIAEFARNAAIANLEGNNFNIIYVEAFKEWEDP 120
 DB 61 DFVWGVGSQWDAFLVQTEQLINERIAEFARNAAIANLEGNNFNIIYVEAFKEWEDP 120
 QY 121 NNPATRTRVIDFRILDLGLERDIPSFRISSGFEVPLLSVYAAQANHLAILRDSVIFGER 180
 DB 121 NNPATRTRVIDFRILDLGLERDIPSFRISSGFEVPLLSVYAAQANHLAILRDSVIFGER 180
 QY 181 WGLTTINNVNENRILRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
 DB 181 WGLTTINNVNENRILRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVL 240
 QY 241 DIAAFPNYDNRYPPIQVQQLTREYVTDPLINFNPQLQSVLAQLPTFNVMESSAIRNPHL 300
 DB 241 DIAAFPNYDNRYPPIQVQQLTREYVTDPLINFNPQLQSVLAQLPTFNVMESSAIRNPHL 300
 QY 301 FDILNNLITFTDFWVGGRFYWGGRHVITSSLLICGGNITSPIYGREANQEPFRSFTFNGPV 360
 DB 301 FDILNNLITFTDFWVGGRFYWGGRHVITSSLLICGGNITSPIYGREANQEPFRSFTFNGPV 360

QY 361 FRTLSIPTURLLQQPCQRHHFNLRGGEVGFSTPTNSFTYRGRGTVDLSLTELPPEDNSVP 420
 DB 361 FRTLSIPTURLLQQPWPAPPFNLRGGEVGFSTPTNSFTYRGRGTVDLSLTELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVQRSCTPFLTTGCVFWSWTHRSATLTNTIDPERINQIPLVKGRVWG 480
 DB 421 PREGYSHRLCHATFVQRSCTPFLTTGCVFWSWTHRSATLTNTIDPERINQIPLVKGRVWG 480
 QY 481 GTSVITGPGTGGDILLRNTFGDFVSLQVNIINSPIQRYRLFRYASSRDARVILVTGAA 540
 DB 481 GTSVITGPGTGGDILLRNTFGDFVSLQVNIINSPIQRYRLFRYASSRDARVILVTGAA 540
 QY 541 STGVGQVSVNMPLOKTMIEIGENLTSRTFRYTDFSNPFSPFRANPDIIIGISEQPLFGAGSI 600
 DB 541 STGVGQVSVNMPLOKTMIEIGENLTSRTFRYTDFSNPFSPFRANPDIIIGISEQPLFGAGSI 600
 QY 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
 DB 601 SSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDQVSNLV 660
 QY 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDITIQGGD 720
 DB 661 DCLSDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSGTDITIQGGD 720
 QY 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKAYTRYELRGYIEDSQDLEIYLIRYNAKH 780
 DB 721 DVFKENYVTLPGTVDECYPTLYQKIDESKLYKAYTRYELRGYIEDSQDLEIYLIRYNAKH 780
 QY 781 EIVNVPGTGLWPLSAQSPIGKGPNCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPGTGLWPLSAQSPIGKGPNCAPHLEWNPDLDCSC 823

RESULT 14

AA117790
 ID AAY17790 standard; Protein; 1189 AA.

AC AAY17790;

DT 12-AUG-1999 (first entry)

XX B. thuringiensis crystal protein Cry1C-R180A protein sequence.

KW Bacillus thuringiensis; delta-endotoxin; insecticide; crystal protein;
 KW lepidopteran insect; Cry1C; genetic engineering; mutagenesis; mutant;
 KW caterpillar; beetle; mosquito; toxic; modification.

OS Bacillus thuringiensis.

OS Synthetic.

PN US5914318-A.

PD 22-JUN-1999.

PF 26-NOV-1997; 97US-0980071.

PR 26-NOV-1997; 97US-0980071.

PR 27-NOV-1996; 96US-0757536.

XX (ECOG-) ECOGEN INC.

XX Baum JA, Gilmer AJ, Mettuss AL;

XX WPI; 1999-370510/31.

DR N-PSDB; AAX80036.

XX New modified delta-endotoxin crystal proteins from Bacillus
 PT thuringiensis are useful in insecticidal compositions

XX Example 13; Column 88-90; 144pp; English.

XX The present invention describes a new composition comprising an isolated

CC polypeptide for modified *Bacillus thuringiensis* crystal proteins (CryIC).
 CC The polypeptide of the composition is insecticidally-active against
 CC Lepidoptera. The composition is toxic to an insect cell and comprised
 CC within an insecticidal formulation can be used as a plant protective
 CC spray which is toxic to caterpillars, beetles and mosquitoes. The
 CC polypeptide of the composition may be used to kill an insect through
 CC ingestion of the composition directly or by ingestion of a plant coated
 CC with the composition or a transgenic plant that expresses the polypeptide
 CC composition. The insecticidal proteins produced by *B. thuringiensis* are
 CC harmless to plants and other non-targeted organisms but toxic to their
 CC specific target insect. The polypeptides have improved toxicity so a
 CC reduced amount of bioinsecticide per unit area of treated crop can be
 CC used allowing economic and efficient utilization in the field. The
 CC present sequence represents a modified *B. thuringiensis* crystal protein.
 XX Sequence 1189 AA;
 SQ
 Query Match 98.4%; Score 4288; DB 20; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MEENNQCIPYNCISNPEEVLDOGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPYNCISNPEEVLDOGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVNGIVGPSQMDAFLVQIEQLINERIAEFAARNAANLEGLGNFNFIYVEAFKWEEDP 120
 DB 61 DFVNGIVGPSQMDAFLVQIEQLINERIAEFAARNAANLEGLGNFNFIYVEAFKWEEDP 120
 QY 121 NNPAITRVIDRFRILDLGLLERRIPSPRISGFVEPLLSVYQAANLHLAIRDVSIFGER 180
 DB 121 NNPAITRVIDRFRILDLGLLERRIPSPRISGFVEPLLSVYQAANLHLAIRDVSIFGER 180
 QY 181 WGLTTINVENNRLIRHIDYADHCANTYNGRLNLPKSTYQDWITYNRLRRDLTLVL 240
 DB 181 WGLTTINVENNRLIRHIDYADHCANTYNGRLNLPKSTYQDWITYNRLRRDLTLVL 240
 QY 241 DIAAFFPNYDNRYPPIQPVGQLTREVTDPPLNFNPQLQSVQALPTFNWESSAIRNPHL 300
 DB 241 DIAAFFPNYDNRYPPIQPVGQLTREVTDPPLNFNPQLQSVQALPTFNWESSAIRNPHL 300
 QY 301 FDILNLTITFDWESVGRNPFVNGGHRVVISLIGGNTSPIYGREANQEPSPFTFNGPV 360
 DB 301 FDILNLTITFDWESVGRNPFVNGGHRVVISLIGGNTSPIYGREANQEPSPFTFNGPV 360
 QY 361 FRTLSTPLTLLOQPCORHFNLRGGEGVEFTPTNSFTYGRGTVDLSITELPPEDNSVP 420
 DB 361 FRTLSTPLTLLOQPCORHFNLRGGEGVEFTPTNSFTYGRGTVDLSITELPPEDNSVP 420
 QY 421 PREGYSHRLCHATFVORSSTPFLITGVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
 DB 421 PREGYSHRLCHATFVORSSTPFLITGVVFSWTHRSATLNTIDPERINQIPLVKGFRVMG 480
 QY 481 GTSVITGPGTGDILRRNTGDFVSLQVNNINSPTQRYRLRFYASSRDAIVILTGAA 540
 DB 481 GTSVITGPGTGDILRRNTGDFVSLQVNNINSPTQRYRLRFYASSRDAIVILTGAA 540
 QY 541 STGVGGQVSNVNPLOKTMIEIGENLTSTRTFYTDSPFNPFSSFRANPDIIIGISEQPLFGAGSI 600
 DB 541 STGVGGQVSNVNPLOKTMIEIGENLTSTRTFYTDSPFNPFSSFRANPDIIIGISEQPLFGAGSI 600
 QY 601 SSGELYDKIEILLADATFEAESDLERAQKAVNALFTSSNOIGLTKTDVTDYHIDQVSNLV 660
 DB 601 SSGELYDKIEILLADATFEAESDLERAQKAVNALFTSSNOIGLTKTDVTDYHIDQVSNLV 660
 QY 661 DCLSDFECLDKRELSEKVKHAKLSDEKNLLODPNFRGNNRQDRGWSGTDTIIOGGD 720
 DB 661 DCLSDFECLDKRELSEKVKHAKLSDEKNLLODPNFRGNNRQDRGWSGTDTIIOGGD 720
 QY 721 DVFKNVTLPGTVDECPTVLYOKIDESKLYATRYELRGYIEDSDQLEIYLIRYNAKH 780
 DB 721 DVFKNVTLPGTVDECPTVLYOKIDESKLYATRYELRGYIEDSDQLEIYLIRYNAKH 780

QY 781 EIVNVPGTSLWPLSAQSPIGKCGEPCNRCAPHLEWNPDLDCSC 823
 DB 781 EIVNVPGTSLWPLSAQSPIGKCGEPCNRCAPHLEWNPDLDCSC 823
 RESULT 15
 ID AAY17788 standard; Protein; 1189 AA.
 AC AAY17788;
 AC AAY17788;
 DT 12-AUG-1999 (first entry)
 DE B. thuringiensis crystal protein CryIC-R148A protein sequence.
 KW *Bacillus thuringiensis*; delta-endotoxin; insecticide; crystal protein;
 KW lepidopteran insect; CryIC; genetic engineering; mutagenesis; mutant;
 KW caterpillar; beetle; mosquito; toxic; modification.
 OS *Bacillus thuringiensis*.
 OS Synthetic.
 XX US5914318-A.
 XX 22-JUN-1999.
 XX 26-NOV-1997; 97US-0980071.
 XX 26-NOV-1997; 97US-0980071.
 XX 27-NOV-1996; 96US-0757536.
 XX (ECOG-) ECOGEN INC.
 XX Baum JA, Gilmer AJ, Mettue AL;
 XX WPI; 1999-370510/31.
 XX N-PSDB; AAX80019.
 PT New modified delta-endotoxin crystal proteins from *Bacillus*
 PT thuringiensis are useful in insecticidal compositions
 XX Example 5; Column 83-85; 144pp; English.
 PS The present invention describes a new composition comprising an isolated
 CC polypeptide for modified *Bacillus thuringiensis* crystal proteins (CryIC).
 CC The polypeptide of the composition is insecticidally-active against
 CC lepidoptera. The composition is toxic to an insect cell and comprised
 CC within an insecticidal formulation can be used as a plant protective
 CC spray which is toxic to caterpillars, beetles and mosquitoes. The
 CC polypeptide of the composition may be used to kill an insect through
 CC ingestion of the composition directly or by ingestion of a plant coated
 CC with the composition or a transgenic plant that expresses the polypeptide
 CC composition. The insecticidal proteins produced by *B. thuringiensis* are
 CC harmless to plants and other non-targeted organisms but toxic to their
 CC specific target insect. The polypeptides have improved toxicity so a
 CC reduced amount of bioinsecticide per unit area of treated crop can be
 CC used allowing economic and efficient utilization in the field. The
 CC present sequence represents a modified *B. thuringiensis* crystal protein.
 XX Sequence 1189 AA;
 Query Match 98.4%; Score 4288; DB 20; Length 1189;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 814; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MEENNQCIPYNCISNPEEVLDOGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60
 DB 1 MEENNQCIPYNCISNPEEVLDOGERISTGNSIDISLSLVQFLVSNFVPGGFLVGLI 60
 QY 61 DFVNGIVGPSQMDAFLVQIEQLINERIAEFAARNAANLEGLGNFNFIYVEAFKWEEDP 120
 DB 61 DFVNGIVGPSQMDAFLVQIEQLINERIAEFAARNAANLEGLGNFNFIYVEAFKWEEDP 120

Qy 121 NNPATRTRVIDRRIILDCGLERDIPSPRISGFEVPLLSVYQAANLHLAILRDSVIFGER 180
Db |||||
121 NNPATRTRVIDRRIILDCGLERDIPSPRISGFEVPLLSVYQAANLHLAILRDSVIFGER 180
Qy 181 WGLTTINVENYNRILRHIDEYADHCANTYNRGLNLPKSTYQDWITTYNRLRDLTLTVL 240
Db |||||
181 WGLTTINVENYNRILRHIDEYADHCANTYNRGLNLPKSTYQDWITTYNRLRDLTLTVL 240
Qy 241 DIAAFPENYDNRYPQPVQQLTREVYTDPLINFNPOLQSVQALPTFNWMESSAIRNPHL 300
Db |||||
241 DIAAFPENYDNRYPQPVQQLTREVYTDPLINFNPOLQSVQALPTFNWMESSAIRNPHL 300
Qy 301 FDLINNLTIETDWFSGVGRNFYWGHRVSSLI CGGNITSPDIYCREANQEPFRSFTNGPV 360
Db |||||
301 FDLINNLTIETDWFSGVGRNFYWGHRVSSLI CGGNITSPDIYCREANQEPFRSFTNGPV 360
Qy 361 FRTLSPPTLLQOPCORHFNLRGGEGVEFSTPTNSFTYRGRTVDSLTTELPEDNSVP 420
Db |||||
361 FRTLSPPTLLQOPCORHFNLRGGEGVEFSTPTNSFTYRGRTVDSLTTELPEDNSVP 420
Qy 421 PREGYSHRLCHATFVQRSCTPFLTGTGVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG 480
Db |||||
421 PREGYSHRLCHATFVQRSCTPFLTGTGVFSWTHRSATLTNTIDPERINQIPLVKGFVRWG 480
Qy 481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSINSPIQRYRLRFRYASSRDARVIVLTGAA 540
Db |||||
481 GTSVITGPGTGGDILRRNTFGDFVSLQVNSINSPIQRYRLRFRYASSRDARVIVLTGAA 540
Qy 541 STGVGQGVSNMPLQKTMIEGENLTSTRTPTDPSNPFSFRANPDIIGISEQPLFGAGSI 600
Db |||||
541 STGVGQGVSNMPLQKTMIEGENLTSTRTPTDPSNPFSFRANPDIIGISEQPLFGAGSI 600
Qy 601 SSGELYDKIEIILADATFEAESDLERAKAVNALFTSSNQIGLKTVDYDIDQVSNLV 660
Db |||||
601 SSGELYDKIEIILADATFEAESDLERAKAVNALFTSSNQIGLKTVDYDIDQVSNLV 660
Qy 661 DCLSDFECLDEKRELSKVKHAKRLSDERNLLODPNFRGINROPDRGWRGSTDTITIQGD 720
Db |||||
661 DCLSDFECLDEKRELSKVKHAKRLSDERNLLODPNFRGINROPDRGWRGSTDTITIQGD 720
Qy 721 DVFKENVTLPGTVDSCYPTLYQKIDESKIKAYTRYELRGYIEDSQDLEIYLIRYNAKH 780
Db |||||
721 DVFKENVTLPGTVDSCYPTLYQKIDESKIKAYTRYELRGYIEDSQDLEIYLIRYNAKH 780
Qy 781 EIVNVFPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823
Db |||||
781 EIVNVFPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC 823

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